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- GRAY SCALE DOCUMENTS

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'REGISTRY' ENTERED AT 12:05:21 ON 30 AUG 2002
L1
              918 S [EG] [AT] [GV] [WG] [PS] S/SQSP
    FILE HCAPLUS! ENTERED AT 12:06:28 ON 30 AUG 2002
              491 S L1
L2
L3
                7 S L2 AND MICROTI
     ANSWER 1 OF 7 HCAPLUS COPYRIGHT 2002 ACS
T.3
                             2001:833517 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                             135:367756
                             Babesia microti antigens and methods
TITLE:
                             for the diagnosis and treatment of Babesia
                             microti infection
                             Reed, Steven G.; Lodes, Michael J.; Houghton,
INVENTOR(S):
                             Raymond L.; Sleath, Paul R.; McNeill, Patricia
                             D.; Homer, Mary J.; Secrist, Heather
                             Corixa Corporation, USA
PATENT ASSIGNEE(S):
SOURCE:
                             PCT Int. Appl., 195 pp.
                             CODEN: PIXXD2
DOCUMENT TYPE:
                             Patent
                             English
LANGUAGE:
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
                          KIND
                                 DATE
                                                   APPLICATION NO.
     PATENT NO.
      _____
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                                 20011115
     WO 2001085947
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PRIORITY APPLN. INFO.:
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                                                                    A2 19990405
                                               US 2000-528784
                                                                    A2 20000317
                                               WO 2000-US9136
                                                                    A2 20000405
      Compds. and methods for the diagnosis and treatment of B.
AΒ
      microti infection are disclosed. The compds. provided
      include polypeptides that contain at least one antigenic portion of
    a B. microti antigen and DNA sequences encoding such
      polypeptides. Antigenic epitopes of such antigens are also
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Searcher: Shears 308-4994

provided, together with pharmaceutical compns. and immunogenic

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compns. comprising such polypeptides, DNA sequences or antigenic epitopes. Diagnostic kits contg. such polypeptides, DNA sequences or antigenic epitopes and a suitable detection reagent may be used for the detection of B. microti infection in patients and biol. samples. Antibodies directed against such polypeptides and antigenic epitopes are also provided. 206205-11-0, Antigen BMNI-1 (Babesia microti) 206205-12-1, Antigen BMNI-2 (Babesia microti) 206205-13-2, Antigen BMNI-3 (Babesia microti) 206205-16-5, Antigen BMNI-6 (Babesia microti) 206205-20-1, Antigen BMNI-12 (Babesia microti) 206205-21-2, Antigen BMNI-13 (Babesia microti) 206205-23-4, Antigen BMNI-16 (Babesia microti) RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (amino acid sequence; of Babesia microti antigens used in diagnosis and treatment of Babesia microti infection) 206205-33-6 206205-35-8 206205-36-9 227296-22-2 227296-23-3 227296-26-6 227296-30-2 227296-31-3 227296-32-4 227296-33-5 227296-34-6 227296-35-7, Antigen MN2 (Bombesia microtia fragment) 227296-36-8 227296-37-9, Antigen MN3 (Bombesia microtia fragment) RL: PRP (Properties) (unclaimed protein sequence; babesia microti antigens and methods for the diagnosis and treatment of Babesia microti infection) 205488-48-8 205488-54-6 334074-87-2 334074-88-3 334074-89-4 334074-90-7 RL: PRP (Properties) (unclaimed sequence; babesia microti antigens and methods for the diagnosis and treatment of Babesia microti infection) ANSWER 2 OF 7 HCAPLUS COPYRIGHT 2002 ACS 2001:748300 HCAPLUS ACCESSION NUMBER: 135:299589 DOCUMENT NUMBER: TITLE: Nucleic acids and proteins for the diagnosis and treatment of Babesia microti infection Reed, Steven G.; Lodes, Michael J.; Houghton, INVENTOR(S): Raymond L.; Sleath, Paul R.; McNeill, Patricia D. PATENT ASSIGNEE(S): USA SOURCE: U.S. Pat. Appl. Publ., 26 pp., Cont.-in-part of U. S. Ser. No. 685,436. CODEN: USXXCO DOCUMENT TYPE: Patent LANGUAGE: English FAMILY ACC. NUM. COUNT: PATENT INFORMATION:

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US	2001029295	A1	20011011	US 2000-737178	20001213
US	6306396	B1	20011023	US 1996-723142	19961001
US	6183976	B1	20010206	US 1997-845258	19970424
US	6214971	B1	20010410	US 1997-990571	19971211

308-4994 Shears

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             HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT,
             RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
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             TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
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                                                           A2 19961001
PRIORITY APPLN. INFO.:
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                                                           A2 19981211
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                                                           A2 19990405
                                         US 2000-528784
                                                           A2 20000317
                                         WO 2000-US9136
                                                           A2 20000405
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                                                           Α
                                                              20001213
                                         US 2001-794764
                                                           Α
                                                              20010226
     Compds. and methods for the diagnosis and treatment of B.
AB
    microtiinfection are disclosed. The compds. provided include
     polypeptides that contain at least one antigenic portion of a B.
    microtiantigen and DNA sequences encoding such polypeptides.
    Antigenic epitopes of such antigens are also provided, together with
     pharmaceutical compns. and immunogenic compns. comprising such
     polypeptides, DNA sequences or antigenic epitopes. Diagnostic kits
     contg. such polypeptides, DNA sequences or antigenic epitopes and a
     suitable detection reagent may be used for the detection of B.
    microtiinfection in patients and biol. samples. Antibodies directed
     against such polypeptides and antigenic epitopes are also provided.
IT
     206205-36-9
     RL: BPR (Biological process); BSU (Biological study, unclassified);
     PRP (Properties); BIOL (Biological study); PROC (Process)
        (nucleic acids and proteins for the diagnosis and treatment of
        Babesia microti infection)
IT
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     Antigen MN2 (Bombesia microtia fragment) 227296-36-8
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227296-37-9, Antigen MN3 (Bombesia microtia fragment) 334074-87-2 334074-88-3 334074-89-4 334074-90-7

RL: PRP (Properties)

(unclaimed protein sequence; nucleic acids and proteins for the diagnosis and treatment of Babesia microti infection)

L3 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 2002 ACS ACCESSION NUMBER: 2001:255942 HCAPLUS

DOCUMENT NUMBER: 134:294507

TITLE: Compounds and methods for the diagnosis and

treatment of Babesia microti infection

INVENTOR(S): Reed, Steven G.; Lodes, Michael J.; Houghton,

Raymond

PATENT ASSIGNEE(S): Corixa Corporation, USA

SOURCE: U.S., 78 pp., Cont.-in-part of U.S. Ser. No.

845,258.

CODEN: USXXAM

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

PA	TENT	NO.		KI	ND	DATE				API	PLI	CATI	ON NO	٥.	DATE		
US US	6214 6306 6183	396 976		B B	1 1	2001 2001	1023 0206			US US	19 19	96-7 97-8		2 8	1997 1996 1997	1001 0424	
WO	W:	AU,	CA,	JP,	MX,	NZ							S264		1998 IT,		MC.
	144.	•	PT,	•	01,	21,	Ditty	20,		., -		GD,	011,	,	,	20,	,
AU	9918	204		A	1	1999	0628			ΑU	19	99-1	8204		1998	1211	
US	2001	0292	95	A.	1	2001	1011			US	20	00-7	3717	8	2000	1213	
PRIORIT	Y APP	LN.	INFO	. :				Į	JS	199	96-	7231	42	A2	1996	1001	
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															1997		
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											-	5690			2000		
									-			6057			2000		
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											-	6566			2000		
								τ	JS	200	)O-	6854	36	A2	2000	1010	

AB Compds. and methods for the diagnosis and treatment of Babesia microti infection are disclosed. The compds. provided include polypeptides that contain at least one antigenic portion of a B. microti antigen and DNA sequences encoding such polypeptides. Antigenic epitopes of such antigens are also provided, together with pharmaceutical compns. and vaccines comprising such polypeptides, DNA sequences or antigenic epitopes. Diagnostic kits contg. such polypeptides, DNA sequences or antigenic epitopes and a suitable detection reagent may be used for the detection of B. microti infection in patients and biol. samples. Antibodies directed against such polypeptides and antigenic epitopes are also provided.

IT 206205-11-0 206205-12-1 206205-13-2

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206205-16-5 206205-20-1 206205-21-2
    206205-23-4
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        treatment of Babesia microti infection)
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ΤТ
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        (unclaimed protein sequence; compds. and methods for the
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TΤ
     334074-89-4 334074-90-7
     RL: PRP (Properties)
        (unclaimed sequence; compds. and methods for the diagnosis and
        treatment of Babesia microti infection)
                               THERE ARE 13 CITED REFERENCES AVAILABLE
REFERENCE COUNT:
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    ANSWER 4 OF 7 HCAPLUS COPYRIGHT 2002 ACS
L3
                         2001:91448 HCAPLUS
ACCESSION NUMBER:
                         134:158493
DOCUMENT NUMBER:
                         Nucleic acids and proteins for the diagnosis and
TITLE:
                         treatment of Babesia microti infection
                         Reed, Steven G.; Lodes, Michael J.; Houghton,
INVENTOR(S):
                         Raymond; Sleath, Paul R.
                         Corixa Corporation, USA
PATENT ASSIGNEE(S):
                         U.S., 66 pp., Cont.-in-part of U.S. Ser. No.
SOURCE:
                         723,142.
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FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
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                                        US 2000-528784
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Searcher: Shears 308-4994

WO 2000-US9136

A2 20000405

US 2000-569098 A2 20000510 A2 20000627 US 2000-605724 A2 20000907 US 2000-656688 A2 20001010 US 2000-685436 MARPAT 134:158493 OTHER SOURCE(S): Compds. and methods for the diagnosis and treatment of Babesia microti infection are disclosed. The compds. provided include polypeptides that contain at least one antigenic portion of a B. microti antigen and DNA sequences encoding such polypeptides. The DNA sequences encoding B. microti antigens were prepd. by screening a B. microti expression library with sera obtained from patients infected with B. microti. Antigenic epitopes of such antigens are also provided, together with pharmaceutical compns. and vaccines comprising such polypeptides, DNA sequences or antigenic epitopes. Diagnostic kits contg. such polypeptides, DNA sequences or antigenic epitopes and a suitable detection reagent may be used for the detection of B. microti infection in patients and biol. samples. Antibodies directed against such polypeptides and antigenic epitopes are also provided. 205488-48-8 205488-54-6 206205-11-0 ΙT 206205-12-1 206205-13-2 206205-16-5 206205-20-1 206205-21-2 206205-23-4 206205-33-6 206205-35-8 206205-36-9 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses) (amino acid sequence; nucleic acids and proteins for the diagnosis and treatment of Babesia microti infection) THERE ARE 9 CITED REFERENCES AVAILABLE FOR REFERENCE COUNT: THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT ANSWER 5 OF 7 HCAPLUS COPYRIGHT 2002 ACS L3 2000:282570 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: 133:72606 Serological expression cloning of novel TITLE: immunoreactive antigens of Babesia microti Lodes, Michael J.; Houghton, Raymond L.; AUTHOR(S): Bruinsma, Elizabeth S.; Mohamath, Raodoh; Reynolds, Lisa D.; Benson, Darin R.; Krause, Peter J.; Reed, Steven G.; Persing, David H. CORPORATE SOURCE: Corixa Corporation, Seattle, WA, 98104, USA SOURCE: Infection and Immunity (2000), 68(5), 2783-2790 CODEN: INFIBR; ISSN: 0019-9567 American Society for Microbiology PUBLISHER: Journal DOCUMENT TYPE: English LANGUAGE: Increased recognition of the prevalence of human babesiosis in the United States, together with rising concern about the potential for transmission of this infection by blood transfusion, has provided motivation to develop definitive serol. and mol. tests for the causative agent, Babesia microti. To develop more sensitive and specific assays for B. microti, the authors screened a genomic expression library with patient serum pools. This screening resulted in the identification of three classes of

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novel genes and an addnl. two novel, unrelated genes, which together

encode a total of 17 unique B. microti antigens. The first class (BMN1-2 family) of genes encodes seven closely related antigens with a degenerate six-amino-acid repeat that shows limited homol. to Plasmodium sp. merozoite and sporozoite surface antigens. A second class (BMN1-8 family) of genes encodes six related antigens, and the third class (BMN1-17 family) of genes encodes two related antigens. The two remaining genes code for novel and unrelated sequences. Among the three classes of antigens and remaining novel sequences, five were chosen to code for the most immunodominant antigens (BMN1-2, -9, -15, and -17 and MN-10). Western blot anal. with the resulting recombinant proteins indicated that these antigens were targets of humoral immune responses during B. microti infection in humans.

#### 278626-95-2 278626-96-3 278626-97-4 ΙT 278626-98-5 278626-99-6

RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process) (amino acid sequence; serol. expression cloning of novel

immunoreactive antigens of Babesia microti)

REFERENCE COUNT: THERE ARE 36 CITED REFERENCES AVAILABLE 36 FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

ANSWER 6 OF 7 HCAPLUS COPYRIGHT 2002 ACS T.3 1999:388301 HCAPLUS ACCESSION NUMBER:

131:85409 DOCUMENT NUMBER:

Antigen and gene sequences for diagnosis and TITLE:

treatment of Babesia microti infection

Reed, Steven G.; Lodes, Michael J.; Houghton, Raymond; Sleath, Paul R.; Persing, David; INVENTOR(S):

Bruinsma, Elizabeth

Corixa Corporation, USA; Mayo Foundation for PATENT ASSIGNEE(S):

Medical Education and Research

SOURCE: PCT Int. Appl., 126 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PA	ATENT	NO.		KI	ND	DATE				AP	PLI	CATI	ON N	٥.	DATE		
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r10	6214	•	PT,	SE B	1	2001	0410			ΠC	1 0	97_9	9057	1	1997	1211	
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PRIORI:	ry APP	LN.	INFO	. :								7231	-		1996		
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									-			US91			2000		
												5690 6057			2000 2000		

US 2000-656688 A2 20000907 US 2000-685436 A2 20001010 Compds. and methods for the diagnosis and treatment of Babesia AB microti infection are disclosed. The compds. provided include polypeptides that contain at least one antigenic portion of a B. microti antigen and DNA sequences encoding such polypeptides. Nine antigens share some homol., contain a degenerate repeat of six amino acids with 9-22 repeats occurring in each antigen, and bear some similarity to a Plasmodium falciparum merozoite surface antigen gene. A second group of five antigens bear some homol. to each other but do not show homol. to any previously identified sequences. Two synthetic peptides (BABS-1 and BABS-4) were made to the repeat region of isolated B. microti antigen BMNI-3. Twelve BMNI-6 homologs were obtained from hamster and human patients. Antigenic epitopes of such antigens are also provided, together with pharmaceutical compns. and vaccines comprising such polypeptides, DNA sequences or antigenic epitopes. Diagnostic kits contg. such polypeptides, DNA sequences or antigenic epitopes and a suitable detection reagent may be used for the detection of B. microti infection in patients and biol. samples. Antibodies directed against such polypeptides and antigenic epitopes are also provided. ΙT 205488-48-8 RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (BABS-1 peptide fragment of repeat region of BMNI-3; antigen and gene sequences for diagnosis and treatment of Babesia microti infection) IT 205488-54-6 RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (BABS-4 peptide fragment of repeat region of BMNI-3; antigen and gene sequences for diagnosis and treatment of Babesia microti infection) 206205-11-0 206205-12-1 206205-13-2 IT 206205-16-5 206205-20-1 206205-21-2 206205-33-6 206205-35-8 227296-22-2 227296-23-3 227296-26-6 227296-30-2 227296-31-3 227296-32-4 227296-33-5 227296-34-6 227296-35-7, Antigen MN2 (Bombesia microtia fragment) 227296-36-8 227296-37-9, Antigen MN3 (Bombesia microtia fragment) RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses) (amino acid sequence; antigen and gene sequences for diagnosis and treatment of Babesia microti infection) THERE ARE 3 CITED REFERENCES AVAILABLE FOR REFERENCE COUNT: 3 THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT ANSWER 7 OF 7 HCAPLUS COPYRIGHT 2002 ACS ACCESSION NUMBER: 1998:229027 HCAPLUS 128:292989 DOCUMENT NUMBER: TITLE: Antigens of Babesia microtia and their use in the diagnosis and treatment of infection Reed, Steven G.; Lodes, Michael J.; Houghton, INVENTOR(S):

Ann Carlotte 1 11 11 11 1

Raymond; Sleath, Paul R.

PATENT ASSIGNEE(S): Corixa Corp., USA

SOURCE: Eur. Pat. Appl., 113 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

PATENT	NO.	KIND	DATE	APPLICATION NO.	DATE
EP 8345	67	A2	19980408	EP 1997-117067	19971001
EP 8345	67	A3	19990331		
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	PT, IE,	FI			
US 6306	396	B1	20011023	US 1996-723142	19961001
US 6183	976	B1	20010206		19970424
PRIORITY APP	LN. INFO	. :		US 1996-723142 A	19961001
				US 1997-845258 A	19970424

AB Antigens and epitopes of Babesia microti that can be used in the diagnosis and treatment of infection are described. Genes for the antigens or antibodies against them can be used in the detection of B. microti. CDNAS for these antigens were cloned by screening an expression library in .lambda.ZAP with antiserum to B. microti.

IT 205488-48-8 205488-54-6 206205-11-0 206205-12-1 206205-13-2 206205-16-5 206205-20-1 206205-21-2 206205-23-4 206205-33-6 206205-35-8 206205-36-9

RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(amino acid sequence; antigens of Babesia microtia and their use in diagnosis and treatment of infection)

### E1 THROUGH E32 ASSIGNED

FILE \*REGISTRY\* ENTERED AT 12:07:45 ON 30 AUG 2002

L4 32 SEA FILE=REGISTRY ABB=ON PLU=ON (205488-48-8/BI OR 205488-54-6/BI OR 206205-11-0/BI OR 206205-12-1/BI OR 206205-13-2/BI OR 206205-16-5/BI OR 206205-20-1/BI OR 206205-21-2/BI OR 206205-33-6/BI OR 206205-35-8/BI OR 206205-36-9/BI OR 206205-23-4/BI OR 227296-36-6/BI OR 227296-30-2/BI OR 227296-31-3/BI OR 227296-32-4/BI OR 227296-34-6/BI OR 227296-35-7/BI OR 227296-36-8/BI OR 227296-37-9/BI OR 227296-22-2/BI OR 227296-23-3/BI OR 227296-33-5/BI OR 334074-87-2/BI OR 334074-88-3/BI OR 334074-89-4/BI OR 334074-90-7/BI OR 278626-95-2/BI OR 278626-99-6/BI)

L5 32 L4 AND L1

L5 ANSWER 1 OF 32 REGISTRY COPYRIGHT 2002 ACS

RN **334074-90-7** REGISTRY

CN 90: PN: US6214971 FIGURE: 6 unclaimed sequence (9CI) (CA INDEX NAME)

OTHER NAMES:

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10: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CN
CN
    204: PN: WO0185947 FIGURE: 6 unclaimed sequence
CI
SQL 147
       1 YITLFLMSGA VFAGDTDREA GGPSGTVGPS EAGGPSEAGG PSEAGGPSEA
SEQ
                        51 GGPSEAGGPS EAGGPSHAGG PSEAGGPSGT GWPSEAGWPS EAGWPSEAGW
                           _________
         _____
     101 PSEAGWPSEA GWPSERFGYQ LLWYSRRIVI FNEIYLSHIY EHSVMIL
        _____
        19-66, 73-114
HITS AT:
REFERENCE
        1: 135:367756
REFERENCE 2: 135:299589
REFERENCE 3: 134:294507
    ANSWER 2 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    334074-89-4 REGISTRY
RN
    86: PN: US6214971 FIGURE: 6 unclaimed sequence (9CI) (CA INDEX
CN
    NAME)
OTHER NAMES:
    200: PN: WO0185947 FIGURE: 6 unclaimed sequence
CN
    6: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CN
   MAN
CI
SQL 138
       1 AGDTDREAGG PSGTVGPSSA GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA
SEQ
             51 GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA GGPSEAGWPS EAGWPSEAGG
         ______
     101 PSGTGWPSEA GWPSEAGWPS EAGWPSEAGW PSERFGYQ
        7-18, 25-132
HITS AT:
REFERENCE
        1: 135:367756
REFERENCE 2: 135:299589
REFERENCE
         3: 134:294507
    ANSWER 3 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
RN
    334074-88-3 REGISTRY
    81: PN: US6214971 FIGURE: 6 unclaimed sequence (9CI) (CA INDEX
CN
    NAME)
OTHER NAMES:
    195: PN: WO0185947 FIGURE: 6 unclaimed sequence
CN
CN
    1: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CI
    MAN
SQL 111
       1 GDTDREAGGP SGTVGPSEAG GPSEAGGPSG TVGPSEAGGP SEAGGPSGTG
SEO
             51 WPSEAGGPSG TVGPSEAGGP SEAGGPSGTG WPSGTGWPSE VGWPSERFGY
         101 OLLWYSRRIV I
```

HITS AT: 6-89 REFERENCE 1: 135:367756 135:299589 REFERENCE 2: REFERENCE 3: 134:294507 ANSWER 4 OF 32 REGISTRY COPYRIGHT 2002 ACS L5 334074-87-2 REGISTRY RN 80: PN: US6214971 FIGURE: 6 unclaimed protein (9CI) (CA INDEX NAME) CN OTHER NAMES: CN 194: PN: WOO185947 FIGURE: 6 unclaimed sequence 1: PN: US20010029295 FIGURE: 6A-6B unclaimed protein CN MAN CI SQL 112 1 AGDTDREAGG PSGTVGPSEA GGPSEAGGPS GTVGPSEAGG PSEAGGPSGT SEQ 51 GWPSEAGGPS GTVGPSEAGG PSEAGGPSGT GWPSGTGWPS EVGWPSERFG 101 YQLLWYSRRI VI 7-90 HITS AT: REFERENCE 1: 135:367756 2: 135:299589 REFERENCE REFERENCE 3: 134:294507 ANSWER 5 OF 32 REGISTRY COPYRIGHT 2002 ACS L5 **278626-99-6** REGISTRY RN Antigen BMN1-13 (Babesia microtia strain MN1 clone bmn1-13 precursor) (9CI) (CA INDEX NAME) OTHER NAMES: GenBank AF206524-derived protein GI 7716011 CN MAN CI SQL 262 1 MVSFKSILVP YITLFLMSGA VFASDTDPEA GGPSGTVGPS EAGGPSEAGG SEO 51 PSGTGWPSEA GGPSEAGGPS GTGWPSEAGW SSERFGYQLL PYSRRIVTFN 101 EVCLSYIYKH SVMILERDRV NDGHKDYIEE KTKEKNKLKK ELEKCFPEQY 151 SLMKKEELAR IFDNASTISS KYKLLVDEIS NKAYGTLEGP AADNFDHFRN 201 IWKSIVLKDM FIYCDLLLQH LIYKFYYDNT INDIKKNFDE SKSKALVLRD 251 KITKKDVYVN DH 29-82 HITS AT: REFERENCE 1: 133:72606 ANSWER 6 OF 32 REGISTRY COPYRIGHT 2002 ACS L5278626-98-5 REGISTRY RNAntigen BMN1-7 (Babesia microtia strain MN1 clone bmn1-7 precursor) (9CI) (CA INDEX NAME) OTHER NAMES: CN GenBank AF206250-derived protein GI 7715998 CI

```
SQL 289
       1 MVSFKSILVP YITLFLMSGA VFAGDTDREA GGPSGTVGPS EAGGPSEAGG
SEQ
                                   51 PSEAGGPSEA GGPSEAGGPS EAGGPSEAGG PSGTVGPSEA GGPSEAGGPS
         101 EAGGPSEAGW PSEAGWPSEA GWPSEAGWPS EAGWPSEAGW PSERFGYQLL
         151 WYSRRIVIFN EIYLSHIYEH SVMILERDRV NDGHKDYIEE KTKEKNKLKK
      201 ELEKCFPEQY SLMKKEELAR IIDNASTISS KYKLLVDEIS NKAYGTLEGP
      251 AADDFDHFRN IWKSIVPKNM FLYCDLLLKH LIRLTPRKS
HITS AT: 29-142
REFERENCE 1: 133:72606
    ANSWER 7 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    278626-97-4 REGISTRY
ŔŊ
    Antigen BMN1-6 (Babesia microtia strain MN1 clone bmn1-6 precursor)
    (9CI) (CA INDEX NAME)
OTHER NAMES:
    GenBank AF206249-derived protein GI 7715996
CN
CI
SQL 298
       1 MVSFKSILVP YITLFLMSGA VFAGDTDREA GGPSGTVGPS EAGGPSEAGG
SEO
                                    -- --------- -------
       51 PSEAGGPSEA GGPSEAGGPS EAGGPSEAGG PSEAGGPSGT GWPSEAGWPS
         __________________________________
      101 EAGWPSEAGW PSEAGWPSEA GWPSERFGYQ LLWYSRRIVI FNEIYLSHIY
         151 EHSVMILERD RVNDGHKDYI EEKTKEKNKL KKELEKCFPE QYSLMKKEEL
      201 ARIIDNASTI SSKYKLLVDE ISNKAYGTLE GPAADDFDHF RNIWKSIVPK
      251 NMFLYCDLLL KHLIRKFYCD NTINDIKKNF DDIEKLGCFQ ARSFLPVN
HITS AT: 29-124
REFERENCE 1: 133:72606
    ANSWER 8 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
RN
    278626-96-3 REGISTRY
    Antigen BMN1-3 (Babesia microtia strain MN1 clone bmn1-3 precursor)
    (9CI) (CA INDEX NAME)
OTHER NAMES:
    GenBank AF206245-derived protein GI 7715986
CN
CI
SQL 362
       1 MVSFKSILVP YITLFLMSGA VFASDTDPEA GGPSEAGGPS GTVGPSEAGG
SEO
                                    -- ------
       51 PSEAGGPSGT GWPSEAGGPS EAGGPSEAGG PSEAGGPSGT GWPSGTGWPS
         101 EAGWSSERFG YQLLPYSRRI VIFNEVCLSY IYKHSVMILE RDRVNDGHKD
      151 YIEEKTKEKN KLKKELEKCF PEQYSLMKKE ELARIFDNAS TISSKYKLLV
      201 DEISNKAYGT LEGPAADNFD HFRNIWKSIV LKDMFIYCDL LLQHLIYKFY
      251 YDNTVNDIKK NFDESKSKAL VLRDKITKKD GDYNTHFEDM IKELNSAAEE
      301 FNKIVDIMIS NIGDYDEYDS IASFKPFLSM ITEITKITKV SNVIIPGIKA
      351 LTLTVFLIFI TK
HITS AT: 29-106
```

```
REFERENCE 1: 133:72606
    ANSWER 9 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    278626-95-2 REGISTRY
RN
    Antigen BMN1-2 (Babesia microtia strain MN1 clone bmn1-2 precursor)
CN
          (CA INDEX NAME)
OTHER NAMES:
CN
    GenBank AF206244-derived protein GI 7715984
CI
SQL 326
SEO
        1 MVSFKSILVP YITLFLMSGA VFASDTDPEA GGPSEAGGPS GTVGPSEAGG
                                     51 PSEAGGPSGT VGPSEAGGPS EAGGPSGTGW PSEAGGPSEA GGPSGTVGPS
          101 EAGGPSEAGG PSGTGWPSEA GGPSEAGGPS EAGGPSEAGG PSGTGWPSGT
          151 GWPSEAGWSS ERFGYQLLPY SRRIVIFNEV CLSYIYKHSV MILERDRVND
          _____
      201 GHKDYIEEKT KEKNKLKKEL EKCFPEQYSL MKKEELARIF DNASTISSKY
      251 KLLVDEISNK AYGTLEGPAA DNFDHFRNIW KSIVLKDMFI YCDLLLQHLI
      301 YKFYYDNTVN DIKKNFDESW TQTLKE
HITS AT:
         29-160
REFERENCE 1: 133:72606
    ANSWER 10 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
RN
    227296-37-9 REGISTRY
    Antigen MN3 (Bombesia microtia fragment) (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
    11: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CN
    47: PN: WO0185947 SEQID: 78 unclaimed protein 74: PN: WO0060090 SEQID: 78 unclaimed protein 78: PN: US6214971 SEQID: 78 unclaimed protein
CN
CN
CN
    79: PN: US6214971 SEQID: 79 unclaimed protein
CN
    91: PN: US6214971 FIGURE: 6 unclaimed sequence
CN
    92: PN: US6214971 FIGURE: 6 unclaimed sequence
CN
    Antigen MRT (Bombesia microtia fragment)
CN
CI
    MAN
SQL 120
        1 AGDTDREAGG PSGTVGPSEA GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA
SEO
               51 GGPSEAGGPS EAGGPSEAGG PSGTGWPSEA GWPSEAGWPS EAGWPSEAGW
          101 PSEAGWPSER FGYQLLWYSR
         =======
         7-108
HITS AT:
REFERENCE
         1: 135:367756
REFERENCE
          2: 135:299589
REFERENCE
           3: 134:294507
REFERENCE
         4: 133:295360
```

```
5: 131:85409
REFERENCE
    ANSWER 11 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    227296-36-8 REGISTRY
RN
    Antigen MN1PAT (Bombesia microtia fragment) (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
    46: PN: WOO185947 SEQID: 77 unclaimed protein
CN
    73: PN: WO0060090 SEQID: 77 unclaimed protein
CN
    77: PN: US6214971 SEQID: 77 unclaimed protein
CN
    89: PN: US6214971 FIGURE: 6 unclaimed sequence
CN
    9: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CN
CI
    MAN
SQL
   113
        1 AGDTDREAGG PSGTVGPSEA GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA
SEO
               51 GGPSEAGGPS EAGGPSGTGW PSEAGWPSEA GWPSEAGWPS EAGWPSEAGW
         101 PSERFGYQLL WYS
         7-102
HITS AT:
REFERENCE
         1: 135:367756
REFERENCE
          2:
             135:299589
             134:294507
REFERENCE
          3:
             133:295360
REFERENCE
          4:
          5: 131:85409
REFERENCE
    ANSWER 12 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    227296-35-7 REGISTRY
RN
CN
    Antigen MN2 (Bombesia microtia fragment) (9CI)
                                              (CA INDEX NAME)
OTHER NAMES:
    45: PN: WO0185947 SEQID: 76 unclaimed protein
CN
    72: PN: WO0060090 SEQID: 76 unclaimed protein
CN
    76: PN: US6214971 SEQID: 76 unclaimed protein
CN
    88: PN: US6214971 FIGURE: 6 unclaimed sequence
CN
    8: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CN
    MAN
CI
   94
SQL
SEQ
        1 AGDTDREAGG PSGTVGPSEA GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA
               51 GGPSEAGGPS GTGWPSEAGW PSEAGWPSEA GWPSEAGWPS EAGW
          _____ ____
HITS AT:
         7-90
          1: 135:367756
REFERENCE
REFERENCE
          2:
             135:299589
REFERENCE
          3:
             134:294507
REFERENCE
         4: 133:295360
```

```
REFERENCE 5: 131:85409
    ANSWER 13 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    227296-34-6 REGISTRY
RN
    Antigen MN1HAM (Bombesia microtia fragment) (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
    44: PN: WOO185947 SEQID: 75 unclaimed protein
CN
    71: PN: WO0060090 SEQID: 75 unclaimed protein
CN
    75: PN: US6214971 SEQID: 75 unclaimed protein
CN
    7: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CN
    87: PN: US6214971 FIGURE: 6 unclaimed sequence
CN
CI
    MAN
SQL
   118
       1 AGDTDREAGG PSGTVGPSEA GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA
SEO
              51 GGPSEAGGPS EAGGPSGTGW PSEAGWPSEA GWPSEAGWPS EAGWPSEAGW
         101 PSERFGYQLL WYSRRIVI
         7-102
HITS AT:
          1: 135:367756
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REFERENCE
          2: 135:299589
            134:294507
REFERENCE
          3:
         4: 133:295360
REFERENCE
        5: 131:85409
REFERENCE
    ANSWER 14 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    227296-33-5 REGISTRY
RN
CN
    Antigen RIFS (Bombesia microtia fragment) (9CI)
                                             (CA INDEX NAME)
OTHER NAMES:
    43: PN: WOO185947 SEQID: 74 unclaimed protein
CN
    70: PN: WO0060090 SEQID: 74 unclaimed protein
CN
    74: PN: US6214971 SEQID: 74 unclaimed protein
CN
    MAN
CI
   138
SQL
SEQ
       1 AGDTDREAGG PSGTVGPSEA GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA
              ____ _____
      51 GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA GGPSEAGWPS EAGWPSEAGG
         101 PSGTGWPSEA GWPSEAGWPS EAGWPSEAGW PSERFGYQ
         HITS AT:
         7-132
REFERENCE
          1: 135:367756
REFERENCE
          2: 134:294507
REFERENCE
          3: 133:295360
REFERENCE
         4: 131:85409
```

```
ANSWER 15 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
RN
    227296-32-4 REGISTRY
    Antigen BI2018 (Bombesia microtia fragment) (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
    42: PN: WO0185947 SEQID: 73 unclaimed protein
CN
    5: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CN
    69: PN: WO0060090 SEQID: 73 unclaimed protein
CN
    73: PN: US6214971 SEQID: 73 unclaimed protein
CN
    85: PN: US6214971 FIGURE: 6 unclaimed sequence
CN
    MAN
CI
SQL
   136
        1 GDTDREAGGP SGTVGPSEAG GPSEAGGPSE AGGPSEAGGP SEAGGPSEAG
SEQ
              ____ ______
       51 GPSEAGGPSE AGGPSEAGGP SEAGGPSEAG WPSEAGWPSE AGGPSGTGWP
         __________________
      101 SEAGWPSEAG WPSEAGWPSE AGWPSERFGY QLLWYS
         ______
         6-125
HITS AT:
          1: 135:367756
REFERENCE
REFERENCE
          2:
             135:299589
REFERENCE
          3:
             134:294507
             133:295360
REFERENCE
         4:
REFERENCE
         5: 131:85409
    ANSWER 16 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    227296-31-3 REGISTRY
RN
    Antigen BI2253 (Bombesia microtia fragment) (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
    41: PN: WOO185947 SEQID: 72 unclaimed protein
CN
    4: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CN
    68: PN: WO0060090 SEQID: 72 unclaimed protein
CN
    72: PN: US6214971 SEQID: 72 unclaimed protein
CN
    84: PN: US6214971 FIGURE: 6 unclaimed sequence
CN
    MAN
CI
SQL 116
        1 EAGGPSGTVG PSEAGGPSEA GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA
SEQ
         51 GGPSEAGGPS EAGGPSEAGW PSEAGWPSEA GGPSGTGWPS EAGWPSEAGW
         101 PSEAGWPSEA GWPSER
         -------
HITS AT:
         1-114
REFERENCE
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REFERENCE
          2:
             135:299589
REFERENCE
             134:294507
          3:
REFERENCE
         4: 133:295360
```

```
REFERENCE 5: 131:85409
    ANSWER 17 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
   227296-30-2 REGISTRY
RN
    Antigen BI2259 (Bombesia microtia fragment) (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
    3: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CN
    40: PN: WO0185947 SEQID: 71 unclaimed protein
CN
    71: PN: US6214971 SEQID: 71 unclaimed protein
CN
    83: PN: US6214971 FIGURE: 6 unclaimed sequence
CN
CI
    MAN
   136
SQL
       1 AGDTDREAGG PSGTVGPSEA GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA
SEQ
              ___ _______
       51 GGPSEAGGPS EAGGPSEAGG PSEAGWPSEA GWPSEAGGPS GTGWPSEAGW
         101 PSEAGWPSEA GWPSEAGWPS ERFGYQLLWY SRRIVI
         7-120
HITS AT:
         1: 135:367756
REFERENCE
REFERENCE
        2: 135:299589
REFERENCE 3: 134:294507
REFERENCE 4: 133:295360
REFERENCE 5: 131:85409
    ANSWER 18 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    227296-26-6 REGISTRY
RN
    Antigen BI2227 (Bombesia microtia fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
    2: PN: US20010029295 FIGURE: 6A-6B unclaimed protein
CN
    39: PN: WO0185947 SEQID: 70 unclaimed protein
CN
    67: PN: WO0060090 SEQID: 70 unclaimed protein 70: PN: US6214971 SEQID: 70 unclaimed protein
CN
CN
    82: PN: US6214971 FIGURE: 6 unclaimed sequence
CN
CI
    MAN
   118
SQL
       1 AGDTDREAGG PSGTVGPSEA GGPSEAGGPS EAGGPSEAGG PSEAGGPSEA
SEQ
              51 GGPSEAGGPS EAGGPSEAGG PSEAGWPSEA GWPSEAGGPS GTGWPSEAGW
         101 PSEAGWPSEA GWPSEAGW
         HITS AT:
         7-114
        1: 135:367756
REFERENCE
         2: 135:299589
REFERENCE
REFERENCE
         3: 134:294507
         4: 133:295360
REFERENCE
```

```
5: 131:85409
REFERENCE
    ANSWER 19 OF 32 REGISTRY COPYRIGHT 2002 ACS
    227296-23-3 REGISTRY
    Antiqen BI1053 (Bombesia microtia fragment) (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
    38: PN: WO0185947 SEQID: 69 unclaimed protein
CN
    66: PN: WO0060090 SEQID: 69 unclaimed protein
CN
    69: PN: US6214971 SEQID: 69 unclaimed protein
CN
CI
    MAN
SQL
   105
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SEO
               51 GWPSEAGGPS GTVGPSEAGG PSEAGGPSGT GWPSGTGWPS EVGWPNEPFG
         101 YHLLW
         7-90
HITS AT:
REFERENCE
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          2: 134:294507
REFERENCE
REFERENCE
          3: 133:295360
          4: 131:85409
REFERENCE
    ANSWER 20 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    227296-22-2 REGISTRY
RN
    Antigen BI254 (Bombesia microtia fragment) (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
    37: PN: WO0185947 SEQID: 68 unclaimed protein
CN
    65: PN: WO0060090 SEQID: 68 unclaimed protein
CN
    68: PN: US6214971 SEQID: 68 unclaimed protein
CN
CI
    MAN
SQL
   101
       1 AGDTDREAGG PSGTVGPSEA GGPSEAGGPS GTVGPSEAGG PSEAGGPSGT
SEO
              51 GWPSEAGGPS GTVGPSEAGG PSEAGGPSGT GWPSGTGWPS EVGWPIEPFG
         101 Y
         7-90
HITS AT:
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REFERENCE
          2: 134:294507
          3: 133:295360
REFERENCE
REFERENCE
          4: 131:85409
    ANSWER 21 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
RN
    206205-36-9 REGISTRY
    Antigen (Babesia microtia 367-amino acid) (9CI)
                                               (CA INDEX NAME)
CN
OTHER NAMES:
    18: PN: WO0185947 SEQID: 49 unclaimed protein
CN
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Searcher :

Shears

308-4994

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2: PN: US20010029295 SEQID: 49 claimed protein
CN
    46: PN: WO0060090 SEQID: 49 unclaimed protein
CN
    49: PN: US6183976 SEQID: 49 claimed protein
CN
    49: PN: US6214971 SEQID: 49 unclaimed protein
CN
    Antigen BMNI-3 (Babesia microtia isoform 2 fragment)
CN
    MAN
CI
   367
SQL
SEO
        1 MVSFKSILVP YITLFLMSGA VFASDTDPEA GGPSEAGGPS GTVGPSEAGG
                                     __ _____
       51 PSEAGGPSGT GWPSEAGGPS EAGGPSEAGG PSEAGGPSGT GSEAGGWPSG
         101 TGWPSEAGWS SERFGYOLLP YSRRIVIFNE VCLSYIYKHS VMILERDRVN
          151 DGHKDYIEEK TKEKNKLKKE LEKCFPEQYS LMKKEELARI FDNASTISSK
      201 YKLLVDEISN KAYGTLEGPA ADNFDHFRNI WKSIVLKDMF IYCDLLLQHL
      251 IYKFYYDNTV NDIKKNFDES KSKALVLRDK ITKKDGDYNT HFEDMIKELN
      301 SAAEEFNKIV DIMISNIGDY DEYDSIASFK PFLSMITEIT KITKVSNVII
      351 PGIKALTLTV FLIFITK
         29-88, 100-111
HITS AT:
REFERENCE
         1: 135:367756
REFERENCE
          2: 135:299589
         3: 134:294507
REFERENCE
REFERENCE
         4: 134:158493
             133:295360
REFERENCE
         5:
          6: 128:292989
REFERENCE
    ANSWER 22 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
RN
    206205-35-8 REGISTRY
    Antigen (Babesia microtia 294-amino acid) (9CI)
                                                (CA INDEX NAME)
CN
OTHER NAMES:
    14: PN: WOO185947 SEQID: 46 unclaimed protein
CN
    45: PN: WO0060090 SEQID: 46 unclaimed protein
CN
    46: PN: US6183976 SEQID: 46 claimed protein
CN
    46: PN: US6214971 SEQID: 46 unclaimed protein
CN
    Antigen BMNI-7 (Babesia microtia isoform fragment)
CN
    Antigen BMNI-7 (Bombesia microtia reverse complement fragment)
CN
CI
    MAN
SQL 294
        1 LWFIKMVSFK SILVPYITLF LMSGAVFAGD TDREAGGPSG TVGPSEAGGP
SEO
                                          51 SEAGGPSEAG GPSEAGGPSE AGGPSEAGGP SEAGGPSGTV GPSEAGGPSE
          101 AGGPSEAGGP SEAGWPSEAG WPSEAGWPSE AGWPSEAGWP SEAGWPSERF
          151 GYOLLWYSRR IVIFNEIYLS HIYEHSVMIL ERDRVNDGHK DYIEEKTKEK
      201 NKLKKELEKC FPEQYSLMKK EELARIIDNA STISSKYKLL VDEISNKAYG
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REFERENCE 3: 134:158493
REFERENCE 4: 133:295360
REFERENCE 5: 131:85409
            6: 128:292989
REFERENCE
    ANSWER 23 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    206205-33-6 REGISTRY
RN
    Antigen (Babesia microtia 154-amino acid) (9CI) (CA INDEX NAME)
CN
OTHER NAMES:
    12: PN: WO0185947 SEQID: 44 unclaimed protein
CN
     43: PN: WO0060090 SEQID: 44 unclaimed protein
CN
     44: PN: US6183976 SEQID: 44 claimed protein
CN
     44: PN: US6214971 SEQID: 44 unclaimed protein
CN
     Antigen BMNI-5 (Babesia microtia isoform 2 fragment)
CN
     Antigen BMNI-5 (Bombesia microtia reverse complement 154-amino acid
CN
     fragment)
CI
    MAN
SQL 154
         1 LWFIKMVSFK SILVPYITLF LMSGAVFAGD TDREAGGPSG TVGPSEAGGP
SEQ
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     ANSWER 24 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
     206205-23-4 REGISTRY
RN
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     Antigen (Babesia microtia 128-amino acid) (9CI)
CN
OTHER NAMES:
     250: PN: WOO185947 SEQID: 31 claimed protein
CN
     30: PN: WOO060090 SEQID: 31 unclaimed protein 31: PN: US6183976 SEQID: 31 claimed protein 31: PN: US6214971 SEQID: 31 claimed protein
CN
CN
CN
     Antigen BMNI-16 (Babesia microti)
Antigen BMNI-16 (Babesia microtia fragment)
CN
CN
CI
     MAN
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REFERENCE
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    ANSWER 25 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    206205-21-2 REGISTRY
RN
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                                                 (CA INDEX NAME)
CN
OTHER NAMES:
    247: PN: WO0185947 SEQID: 28 claimed protein
CN
    28: PN: US6183976 SEQID: 28 claimed protein
CN
    28: PN: US6214971 SEQID: 28 claimed protein
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    28: PN: WO0060090 SEQID: 28 unclaimed protein
CN
    Antigen BMNI-13 (Babesia microti)
CN
    Antigen BMNI-13 (Babesia microtia fragment)
CN
    Antigen BMNI-13 (Bombesia microtia antigen BMNI-17 fragment)
CN
CI
    MAN
SQL 267
SEQ
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                                           _____
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          101 IVTFNEVCLS YIYKHSVMIL ERDRVNDGHK DYIEEKTKEK NKLKKELEKC
      151 FPEQYSLMKK EELARIFDNA STISSKYKLL VDEISNKAYG TLEGPAADNF
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REFERENCE
           6: 128:292989
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Searcher: Shears 308-4994

ANSWER 26 OF 32 REGISTRY COPYRIGHT 2002 ACS

206205-20-1 REGISTRY

L5 RN

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Antigen (Babesia microtia 121-amino acid) (9CI)
                                                 (CA INDEX NAME)
OTHER NAMES:
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    27: PN: US6214971 SEQID: 27 claimed protein
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    27: PN: WO0060090 SEQID: 27 unclaimed protein
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    Antigen BMNI-12 (Babesia microti)
CN
    Antigen BMNI-12 (Babesia microtia fragment)
CN
    Antigen BMNI-12 (Bombesia microtia antigen BMNI-17 fragment)
CN
CI
SQL
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SEQ
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REFERENCE
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              131:85409
REFERENCE
           6:
              128:292989
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L5
    206205-16-5 REGISTRY
RN
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                                                 (CA INDEX NAME)
CN
OTHER NAMES:
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CN
CN
    23: PN: US6214971 SEQID: 23 claimed protein
CN
    23: PN: WO0060090 SEQID: 23 unclaimed protein
    242: PN: WO0185947 SEQID: 23 claimed protein
CN
CN
    Antigen BMNI-6 (Babesia microti)
CN
    Antigen BMNI-6 (Babesia microtia fragment)
CN
    Antigen BMNI-6 (Bombesia microtia antigen BMNI-17 fragment)
CI
    MAN
SQL
    303
        1 LWFIKMVSFK SILVPYITLF LMSGAVFAGD TDREAGGPSG TVGPSEAGGP
SEQ
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          151 LSHIYEHSVM ILERDRVNDG HKDYIEEKTK EKNKLKKELE KCFPEQYSLM
      201 KKEELARIID NASTISSKYK LLVDEISNKA YGTLEGPAAD DFDHFRNIWK
      251 SIVPKNMFLY CDLLLKHLIR KFYCDNTIND IKKNFDDIEK LGCFQARSFL
      301 PVN
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REFERENCE
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REFERENCE
           5:
               128:292989
REFERENCE
           6:
    ANSWER 28 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    206205-13-2 REGISTRY
RN
    Antigen (Babesia microtia 367-amino acid) (9CI)
                                                   (CA INDEX NAME)
CN
OTHER NAMES:
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CN
    20: PN: US6214971 SEQID: 20 claimed protein
CN
    20: PN: WO0060090 SEQID: 20 unclaimed protein
CN
    239: PN: WO0185947 SEQID: 20 claimed protein
CN
    Antigen BMNI-3 (Babesia microti)
CN
    Antigen BMNI-3 (Babesia microtia fragment)
CN
    Antigen BMNI-3 (Bombesia microtia antigen BMNI-17 fragment)
CN
CI
    MAN
SQL
    367
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SEO
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    ANSWER 29 OF 32 REGISTRY COPYRIGHT 2002 ACS
    206205-12-1 REGISTRY
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    19: PN: US6214971 SEQID: 19 claimed protein
    19: PN: WO0060090 SEQID: 19 unclaimed protein
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    238: PN: WO0185947 SEQID: 19 claimed protein
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CN
CN
    Antigen BMNI-2 (Babesia microtia fragment)
CN
    Antigen BMNI-2 (Bombesia microtia antigen BMNI-17 fragment)
CI
    MAN
SQL
    310
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      201 KKELEKCFPE QYSLMKKEEL ARIFDNASTI SSKYKLLVDE ISNKAYGTLE
      251 GPAADNFDHF RNIWKSIVLK DMFIYCDLLL QHLIYKFYYD NTVNDIKKNF
      301 DESWTQTLKE
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REFERENCE
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REFERENCE
          6:
              128:292989
    ANSWER 30 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
    206205-11-0 REGISTRY
RN
    Antigen (Babesia microtia 263-amino acid) (9CI)
                                                 (CA INDEX NAME)
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CN
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CN
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CN
    Antigen BMNI-1 (Bombesia microtia antigen BMNI-17 fragment)
CN
CI
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SQL
    263
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                131:85409
REFERENCE
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     ANSWER 31 OF 32 REGISTRY COPYRIGHT 2002 ACS
L5
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CN
     serylglycyl-L-threonyl-L-valylglycyl-L-prolyl-L-serylglycyl-L-
     threonylglycyl-L-tryptophyl-L-prolyl-L-seryl-L-.alpha.-glutamyl-L-
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     48: PN: US6214971 SEQID: 48 unclaimed sequence
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                131:85409
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REFERENCE
            6:
    ANSWER 32 OF 32 REGISTRY COPYRIGHT 2002 ACS
L_5
RN
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     L-Serine, L-seryl-L-.alpha.-glutamyl-L-alanylglycylglycyl-L-prolyl-L-
CN
     seryl-L-.alpha.-glutamyl-L-alanylglycylglycyl-L-prolyl-L-serylglycyl-
     L-threonylglycyl-L-tryptophyl-L-threonyl-L-serylglycyl-L-
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                                                             - Author (5)
           4373 S "REED S"?/AU
L6
                                   "LODES M"?/AU
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                                   "HOUGHTON R"?/AU
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123
L23 ANSWER 1 OF 27 HCAPLUS COPYRIGHT 2002 ACS
                                                      DUPLICATE 1
                        2002:275811 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                        136:308523
                        Compositions and methods for WT1 specific
TITLE:
                        immunotherapy
                        Gaiger, Alexander; McNeill, Patricia D.
INVENTOR(S):
                         ; Smithgall, Molly; Moulton, Gus; Vedvick,
                        Thomas S.; Sleath, Paul R.; Mossman,
                        Sally; Evans, Lawrence; Spies, A. Gregory;
                        Boydston, Jeremy
                        Corixa Corporation, USA
PATENT ASSIGNEE(S):
                         PCT Int. Appl., 260 pp.
SOURCE:
                        CODEN: PIXXD2
DOCUMENT TYPE:
                        Patent
                        English
LANGUAGE:
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:
     PATENT NO.
                                          APPLICATION NO.
                     KIND
                           DATE
                                                           DATE
                                           -------
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     WO 2002028414
                      Α1
                            20020411
                                          WO 2001-US31139 20011003
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20020718
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               LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
               NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG,
               KZ, MD, RU, TJ, TM
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               TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN,
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PRIORITY APPLN. INFO.:
                                               US 2000-685830
                                                                   A 20001009
                                               US 2001-785019
                                                                  A 20010215
                                               US 2001-938864
                                                                   A 20010824
     Compns. and methods for the therapy of malignant diseases, such as
ΑB
     leukemia and cancer, are disclosed. The compns. comprise one or
     more of a WT1 polynucleotide, a WT1 polypeptide, an
     antigen-presenting cell presenting a WT1 polypeptide, an antibody
     that specifically binds to a WT1 polypeptide; or a T cell that
     specifically reacts with a WT1 polypeptide. Such compns. may be
     used, for example, for the prevention and treatment of metastatic
     diseases.
                                    THERE ARE 1 CITED REFERENCES AVAILABLE FOR
REFERENCE COUNT:
                             1
                                     THIS RECORD. ALL CITATIONS AVAILABLE IN
                                    THE RE FORMAT
                        HCAPLUS COPYRIGHT 2002 ACS
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L23 ANSWER 2 OF 27
                             2001:833517 HCAPLUS
ACCESSION NUMBER:
                             135:367756
DOCUMENT NUMBER:
                             Babesia microti antigens and methods
TITLE:
                             for the diagnosis and treatment of Babesia
                             microti infection
                             Reed, Steven G.; Lodes, Michael
INVENTOR(S):
                             J.; Houghton, Raymond L.;
                             Sleath, Paul R.; McNeill, Patricia
                             D.; Homer, Mary J.; Secrist,
                             Heather
                             Corixa Corporation, USA
PATENT ASSIGNEE(S):
                             PCT Int. Appl., 195 pp.
SOURCE:
                             CODEN: PIXXD2
DOCUMENT TYPE:
                             Patent
                             English
LANGUAGE:
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
     PATENT NO.
                       KIND DATE
                                                  APPLICATION NO. DATE
                          ____
                                -----
                                                WO 2001-US15192 20010509
                                 20011115
     WO 2001085947
                         A2
              AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
               CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ,
               MD, RU,
                        TJ, TM
          RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
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CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
            TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
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                                       US 2000-656688
                                                        A 20000907
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                                       US 2000-737178
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                                       US 1997-845258
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                                       US 1997-990571
                                                        A2 19971211
                                       WO 1998-US26437 A2 19981211
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                                       US 1999-286488
                                       US 2000-528784
                                                        A2 20000317
                                                        A2 20000405
                                       WO 2000-US9136
    Compds. and methods for the diagnosis and treatment of B.
AΒ
    microti infection are disclosed. The compds. provided
    include polypeptides that contain at least one antigenic portion of
    a B. microti antigen and DNA sequences encoding such
    polypeptides. Antigenic epitopes of such antigens are also
    provided, together with pharmaceutical compns. and immunogenic
    compns. comprising such polypeptides, DNA sequences or antigenic
    epitopes. Diagnostic kits contg. such polypeptides, DNA sequences
    or antigenic epitopes and a suitable detection reagent may be used
    for the detection of B. microti infection in patients and
    biol. samples. Antibodies directed against such polypeptides and
    antigenic epitopes are also provided.
                                                      DUPLICATE 3
L23 ANSWER 3 OF 27 HCAPLUS COPYRIGHT 2002 ACS
                        2001:748300 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                        135:299589
                        Nucleic acids and proteins for the diagnosis and
TITLE:
                        treatment of Babesia microti infection
                        Reed, Steven G.; Lodes, Michael
INVENTOR(S):
                        J.; Houghton, Raymond L.;
                        Sleath, Paul R.; McNeill, Patricia
                        D.
                        USA
PATENT ASSIGNEE(S):
                        U.S. Pat. Appl. Publ., 26 pp., Cont.-in-part of
SOURCE:
                        U. S. Ser. No. 685,436.
                        CODEN: USXXCO
DOCUMENT TYPE:
                        Patent
                        English
LANGUAGE:
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
                     KIND DATE
                                                           DATE
    PATENT NO.
                                          APPLICATION NO.
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                           _____
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                                          US 2000-737178
                           20011011
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    US 2001029295
                      A1
                                                           19961001
    US 6306396
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                           20011023
                                          US 1996-723142
                                          US 1997-845258
                                                           19970424
                     B1
                           20010206
    US 6183976
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                                                           19971211
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    WO 9929869
                     A1
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        W: AU, CA, JP, MX, NZ
        RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC,
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Searcher: Shears 308-4994

NL, PT, SE

20000405

20001012

**A**1

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WO 2000-US9136
    WO 2000060090
            AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN,
             CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,
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             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT,
             RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
             US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
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                    CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
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                                           WO 2001-US15192 20010509
     WO 2001085947
                       A2
                            20011115
            AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
             CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,
             GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,
             LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
             NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR,
             TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ,
             MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
             CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
             TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
             ΤG
                                        US 1996-723142
                                                         A2 19961001
PRIORITY APPLN. INFO.:
                                        US 1997-845258
                                                         A2 19970424
                                                         A2 19971211
                                        US 1997-990571
                                        WO 1998-US26437
                                                         A2 19981211
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                                        US 2000-605724
                                                         A2 20000627
                                                         A2 20000907
                                        US 2000-656688
                                        US 2000-685436
                                                         A2 20001010
                                        US 2000-737178
                                                         A 20001213
                                        US 2001-794764
                                                         A 20010226
AΒ
     Compds. and methods for the diagnosis and treatment of B.
    microtiinfection are disclosed. The compds. provided include
    polypeptides that contain at least one antigenic portion of a B.
    microtiantigen and DNA sequences encoding such polypeptides.
    Antigenic epitopes of such antigens are also provided, together with
    pharmaceutical compns. and immunogenic compns. comprising such
    polypeptides, DNA sequences or antigenic epitopes. Diagnostic kits
     contg. such polypeptides, DNA sequences or antigenic epitopes and a
     suitable detection reagent may be used for the detection of B.
     microtiinfection in patients and biol. samples. Antibodies directed
     against such polypeptides and antigenic epitopes are also provided.
L23 ANSWER 4 OF 27 HCAPLUS COPYRIGHT 2002 ACS
                                                       DUPLICATE 4
                         2001:255942 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                         134:294507
                         Compounds and methods for the diagnosis and
TITLE:
                         treatment of Babesia microti infection
                         Reed, Steven G.; Lodes, Michael
INVENTOR(S):
                         J.; Houghton, Raymond
PATENT ASSIGNEE(S):
                         Corixa Corporation, USA
                         U.S., 78 pp., Cont.-in-part of U.S. Ser. No.
SOURCE:
                         845,258.
                         CODEN: USXXAM
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308-4994 Searcher : Shears

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

		CENT :			KII		DATE			AP	PLIC	CATI	ON NO	٥.	DATE		
		6214					2001	0410		US	199	97-9	9057	1	1997	1211	
	US	6306	396		В:	1	2001	1023		US	199	96-7.	23142	2	1996	1001	
	US	6183	976		B:	1	2001	0206		US	199	97-8	45258	3	19970	0424	
						19990617			WO 1998-US26437 199812					1211			
					JP,												
								DK,	ES,	FI,	FR,	GB,	GR,	ΙE,	IT,	LU,	MC,
					SE		•	•	•		•	•	•	·	•	•	•
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		2001															
PRIOR															1996		
									Ü	S 19	97-8	3452	58	A2	19970	0424	
									Ü	S 19	97-9	9905	71	Α	1997	1211	
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										S 19			-		19990		
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AB	Con	npds.	and	metl	hods	for	the	dia	gnosi	s an	d tı	ceati	ment	of	Babes	sia	

MB Compds. and methods for the diagnosis and treatment of Babesia microti infection are disclosed. The compds. provided include polypeptides that contain at least one antigenic portion of a B. microti antigen and DNA sequences encoding such polypeptides. Antigenic epitopes of such antigens are also provided, together with pharmaceutical compns. and vaccines comprising such polypeptides, DNA sequences or antigenic epitopes. Diagnostic kits contg. such polypeptides, DNA sequences or antigenic epitopes and a suitable detection reagent may be used for the detection of B. microti infection in patients and biol. samples. Antibodies directed against such polypeptides and antigenic epitopes are also provided.

REFERENCE COUNT: 13 THERE ARE

THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L23 ANSWER 5 OF 27 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 5

ACCESSION NUMBER: 2001:91448 HCAPLUS

DOCUMENT NUMBER: 134:158493

TITLE: Nucleic acids and proteins for

Nucleic acids and proteins for the diagnosis and

treatment of Babesia microti infection

INVENTOR(S): Reed, Steven G.; Lodes, Michael

J.; Houghton, Raymond;

Sleath, Paul R.

PATENT ASSIGNEE(S): Corixa Corporation, USA

SOURCE: U.S., 66 pp., Cont.-in-part of U.S. Ser. No.

723,142.

CODEN: USXXAM

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT:

#### PATENT INFORMATION:

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p1 ----
     PATENT NO.
                   KIND DATE
                                              APPLICATION NO. DATE
         R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
              PT, IE, FI
     US 6214971 B1
US 2001029295 A1
                              20010410
                                               US 1997-990571
                                                                 19971211
                                              US 2000-737178 20001213
                              20011011
                                           US 1996-723142 A2 19961001
US 1997-845258 A 19970424
US 1997-990571 A2 19971211
WO 1998-US26437 A2 19981211
PRIORITY APPLN. INFO.:
                                           US 1999-286488 A2 19990405

US 2000-528784 A2 20000317

WO 2000-US9136 A2 20000405

US 2000-569098 A2 20000510

US 2000-65724 A2 20000627

US 2000-656688 A2 20000907

US 2000-685436 A2 20001010
                          MARPAT 134:158493
OTHER SOURCE(S):
     Compds. and methods for the diagnosis and treatment of Babesia
     microti infection are disclosed. The compds. provided
     include polypeptides that contain at least one antigenic portion of
     a B. microti antigen and DNA sequences encoding such
     polypeptides. The DNA sequences encoding B. microti
     antigens were prepd. by screening a B. microti expression
     library with sera obtained from patients infected with B.
     microti. Antigenic epitopes of such antigens are also
     provided, together with pharmaceutical compns. and vaccines
     comprising such polypeptides, DNA sequences or antigenic epitopes.
     Diagnostic kits contg. such polypeptides, DNA sequences or antigenic
     epitopes and a suitable detection reagent may be used for the
     detection of B. microti infection in patients and biol.
     samples. Antibodies directed against such polypeptides and
     antigenic epitopes are also provided.
REFERENCE COUNT:
                           9
                                 THERE ARE 9 CITED REFERENCES AVAILABLE FOR
                                 THIS RECORD. ALL CITATIONS AVAILABLE IN
                                 THE RE FORMAT
L23 ANSWER 6 OF 27 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
                     2002:6260 BIOSIS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                     PREV200200006260
                     Compounds and methods for the diagnosis and treatment
TITLE:
                     of B. microti infection.
AUTHOR(S):
                     Reed, Steven G.; Lodes, Michael J.
                     ; Houghton, Raymond; Sleath, Paul
                     ASSIGNEE: Corixa Corporation
PATENT INFORMATION: US 6306396 October 23, 2001
                     Official Gazette of the United States Patent and
SOURCE:
                     Trademark Office Patents, (Oct. 23, 2001) Vol. 1251,
                     No. 4, pp. No Pagination. e-file.
                     ISSN: 0098-1133.
DOCUMENT TYPE:
                     Patent
```

LANGUAGE: English

Compounds and methods for the diagnosis and treatment of B. AB microti infection are disclosed. The compounds provided include polypeptides that contain at least one antigenic portion of a B. microti antigen and DNA sequences encoding such polypeptides. Antigenic epitopes of such antigens are also provided, together with pharmaceutical compositions and vaccines comprising such polypeptides, DNA sequences or antigenic epitopes. Diagnostic kits containing such polypeptides, DNA sequences or antigenic epitopes and a suitable detection reagent may be used for the detection of B. microti infection in patients and biological samples. Antibodies directed against such polypeptides and antigenic epitopes are also provided.

L23 ANSWER 7 OF 27 WPIDS (C) 2002 THOMSON DERWENT

ACCESSION NUMBER:

2002-062250 [08] WPIDS

CROSS REFERENCE:

1998-609891 [51]; 2000-160675 [11]

DOC. NO. NON-CPI: DOC. NO. CPI:

N2002-046184

TITLE:

C2002-017807

Novel polynucleotide encoding polypeptides useful for detecting Ehrlichia infection in patients and

biological samples, and for treating human

granulocytic ehrlichiosis, comprise an Ehrlichia

antigen.

DERWENT CLASS:

B04 C06 D16 S03

INVENTOR(S):

HOUGHTON, R L; LODES, M J;

MCNEILL, P D; REED, S G

PATENT ASSIGNEE(S):

(CORI-N) CORIXA CORP; (HOUG-I) HOUGHTON R L;

(LODE-I) LODES M J; (MCNE-I) MCNEILL P D; (REED-I)

REED S G

COUNTRY COUNT: 95

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA

WO 2001085949 A2 20011115 (200208)\* EN 132

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC

MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2001059507 A 20011120 (200219) US 2002068343 A1 20020606 (200241)

### APPLICATION DETAILS:

PATENT NO KIND	 APPLICATION	DATE
WO 2001085949 A2 AU 2001059507 A US 2002068343 A1	WO 2001-US14518 AU 2001-59507 US 1997-821324 US 1997-975762 US 1998-106582 US 1998-159469 US 1999-295028 US 2000-566617	20010504 20010504 19970321 19971120 19980629 19980923 19990420 20000508

CIP of US 2000-693542 20001020 US 2001-798042 20010302

FILING DETAILS:

PATENT NO KIND PATENT NO

AU 2001059507 A Based on WO 200185949
US 2002068343 A1 CIP of US 6207169
CIP of US 6231869
CIP of US 6277381
CIP of US 6306402

1 61 3

PRIORITY APPLN. INFO: US 2001-798042 20010302; US 2000-566617 20000508; US 2000-693542 20001020; US 1997-821324 19970321; US 1997-975762 19971120; US 1998-106582 19980629; US 1998-159469 19980923; US 1999-295028 19990420

AN 2002-062250 [08] WPIDS

CR 1998-609891 [51]; 2000-160675 [11]

AB WO 200185949 A UPAB: 20020701

NOVELTY - An isolated polynucleotide (I) comprising a sequence (S1) chosen from 36 nucleotides of defined bp fully in the specification such as 1345, 1132, 554, 559, 201, 467, 530, 1185, 1131, 800, 1011, 513, 464, 527, 464, 860, 484 or 1039 bp, complement of (S1), a sequence hybridizable under moderate stringent conditions to (S1), a sequence which is 75% or 90% identical to (S1) or degenerate variant of (S1), is new.

DETAILED DESCRIPTION - (I) is chosen from the determined DNA sequence of human granulocytic ehrlichiosis (HGE)-1, HGE-3, HGE-6, HGE-8, HGE-11-13, HGE-23, HGE-24, the 5' DNA sequence of HGE-7, HGE-2, HGE-9, HGE-14-18, HGE-25, extended DNA sequences of HGE-2, HGE-7, HGE-8, HGE-11, HGE-14-16, HGE-18, HGE-23, HGE-25, the determined 3' DNA sequence of HGE-17, the full-length cDNA sequence for HGE-17, corrected cDNA sequence for HGE-14, HGE-1, and the reverse complement of HGE-2, HGE-14 and HGE-15. INDEPENDENT CLAIMS are also included for the following:

- (1) an isolated polypeptide ( $\overline{\text{II}}$ ) comprising a sequence encoded by ( $\overline{\text{II}}$ ) or a sequence 70% or 90% identical to a sequence encoded by ( $\overline{\text{II}}$ );
- (2) an isolated antigenic epitope (III) of an Ehrlichia antigen comprising a sequence of 41 or 125 amino acids defined in the specification;
- (3) an isolated polypeptide comprising at least two antigenic epitopes as above;
  - (4) a recombinant expression vector (IV) comprising (I);
  - (5) a host cell (V) transformed with (IV);
  - (6) a fusion protein (VI) comprising (II) or (III);
- (7) a diagnostic kit comprising (II), (III) and (VI) and a detection reagent;
- (8) a diagnostic kit comprising at least two oligonucleotide probes or primer specific for (I);
- (9) an isolated antibody (VII), or its antigen binding fragment that specifically binds to (II) or (III);
- (10) a composition (VIII) comprising any one chosen from (I)-(III), (VI) and (VII), and immunostimulants;
- (11) detecting Ehrlichia infection in a biological sample, by contacting the sample with oligonucleotide primers or probes, or a

binding agent capable of binding to (II), (III) or (VI) and detecting in the sample the presence of amplified polynucleotide sequence, polynucleotide sequence that hybridizes to the probe or polypeptide that binds to the binding agent; and

(12) detecting a disorder of Ehrlichia infection, Lyme disease and B.microti infection in a patient, by contacting the biological sample with (II), a Lyme disease antigen, and a B. microti antigen, and detecting the presence of antibodies in the biological sample that bind to either the polypeptide, Lyme disease antigen or the B.microti antigen.

ACTIVITY - Antibiotic. No supporting data is provided. MECHANISM OF ACTION - Vaccine. No supporting data is given. USE - (II), (III) and (VI) are useful for detecting Ehrlichia infection in a patient. (VIII) is useful for stimulating an immune response in a patient, for treating Ehrlichia infection in a patient (claimed). (II) is useful for serodiagnosis and treatment of human granulocytic ehrlichiosis (HGE). (VII) is useful in diagnostic test to detect the presence of Ehrlichia antigens and for detecting Ehrlichia infection in a patient. Dwg.0/2

SCISEARCH COPYRIGHT 2002 ISI (R) L23 ANSWER 8 OF 27

2001:943909 SCISEARCH ACCESSION NUMBER:

THE GENUINE ARTICLE: 494QP

Innate resistance to Babesia infection is influenced TITLE:

by genetic background and gender

Aguilar-Delfin I; Homer M J; Wettstein P AUTHOR:

J; Persing D H (Reprint)

Corixa Corp, Suite 200, 1124 Columbia St, Seattle, CORPORATE SOURCE:

WA 98104 USA (Reprint); Mayo Clin & Mayo Fdn, Dept Immunol, Rochester, MN 55905 USA; Corixa Corp,

Seattle, WA 98104 USA; Infect Dis Res Inst, Seattle,

WA 98104 USA

COUNTRY OF AUTHOR: USA

SOURCE:

INFECTION AND IMMUNITY, (DEC 2001) Vol. 69, No. 12,

pp. 7955-7958.

Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW,

WASHINGTON, DC 20036-2904 USA.

ISSN: 0019-9567.

DOCUMENT TYPE:

Article; Journal

LANGUAGE:

English

REFERENCE COUNT: 30

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

Infection of severe combined immunodeficient mice with Babesia AΒ sp. strain WA1 was studied to assess the contributions of innate and adaptive immunity in resistance to acute babesiosis. The scid mutation showed little effect in genetically susceptible C3H mice and did not decrease the inherent resistance of C57BL/6 mice to the infection, suggesting that innate immunity plays a central role in determining the course of Babesia infection in these strains. In contrast, the scid mutation dramatically impaired resistance in moderately susceptible BALB/c mice, suggesting that acquired immunity may play an important secondary role. In comparison to their female counterparts, male mice of different genetic backgrounds showed increased resistance to the infection, indicating that the gender of the host may influence protection against babesiosis.

SCISEARCH COPYRIGHT 2002 ISI (R) L23 ANSWER 9 OF 27

2001:546315 SCISEARCH ACCESSION NUMBER:

THE GENUINE ARTICLE: 447RN

Serodiagnosis of human granulocytic ehrlichiosis by TITLE:

using novel combinations of immunoreactive

recombinant proteins

Lodes M J (Reprint); Mohamath R; Reynolds AUTHOR:

L D; McNeill P; Kolbert C P; Bruinsma E S;

Benson D R; Hofmeister E; Reed S G;

Houghton R L; Persing D H

Corixa Corp, 1124 Columbia St, Suite 200, Seattle, CORPORATE SOURCE:

WA 98104 USA (Reprint); Infect Dis Res Inst, Seattle, WA 98104 USA; Corixa Corp, Seattle, WA 98104 USA; Univ Washington, Dept Pathobiol, Seattle, WA 98195 USA; Mayo Clin & Mayo Fdn, Dept Lab Med &

Pathol, Rochester, MN 55905 USA

COUNTRY OF AUTHOR:

JOURNAL OF CLINICAL MICROBIOLOGY, (JUL 2001) Vol. SOURCE:

39, No. 7, pp. 2466-2476.

Publisher: AMER SOC MICROBIOLOGY, 1752 N ST NW,

WASHINGTON, DC 20036-2904 USA.

ISSN: 0095-1137. Article; Journal

DOCUMENT TYPE:

English LANGUAGE:

REFERENCE COUNT:

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

A panel of seven recombinant antigens, derived from Ehrlichia AΒ phagocytophila (the agent of human granulocytic ehrlichiosis), was evaluated by class-specific enzyme-linked immunosorbent assays (ELISAs) for utility in the diagnosis of the infection. Fourteen genomic fragments, obtained by serologic expression screening, contained open reading frames (ORFs) encoding 16 immunodominant antigens, Eleven of these antigens were members of the major surface protein (MSP) multigene family, Alignment of their predicted protein sequences revealed a pattern of conserved sequences, which contained short direct repeats, flanking a variable region. In addition, two genomic clones contained two and three MSP ORFs, respectively, indicating that these genes are clustered in tandem copies. The implications for this pattern of both genomic and protein arrangements in antigenic variations of MSPs and in their utilities in a diagnostic assay are discussed. In addition to two :MSP recombinant antigens (rHGE-1 and -3) and a fusion protein of these antigens (rErf-1), five further recombinants were evaluated by ELISA. Two of these antigens (rHGE-14 and -15) were novel, while a third (rHGE-2), with no known function, has been described. The final two recombinant antigens (rHGE-9 and -17) represent overlapping segments of the ankyrin gene (ank), The addition of rHGE-9 ELISA data resulted in the detection of 78% (21 of 27) of acute-phase sera. When serologic data for all recombinants are combined, 96.2% (26 of 27) of convalescent-phase patient serum samples and 85.2% (23 of 27) of acute-phase patient serum samples are detected, indicating the potential of these antigens for use in the development of a rapid serologic assay for the detection of E. phagocytophila infection.

L23 ANSWER 10 OF 27 SCISEARCH COPYRIGHT 2002 ISI (R)

2001:818201 SCISEARCH ACCESSION NUMBER:

THE GENUINE ARTICLE: 472TV

Peptide ELISA for detection of antibodies to Babesia TITLE:

microti in serum.

Houghton R L (Reprint); Homer M J AUTHOR:

> ; Reynolds L D; Sleath P C; Cable R G; Militscher J E; Lodes M J; Berardi V;

Leiby D A; Persing D H

CORPORATE SOURCE: Corixa Corp, Seattle, WA USA; Amer Red Cross,

Farmington, CT USA; Amer Red Cross, Rockville, MD

USA; Imugen, Norwood, MA USA

COUNTRY OF AUTHOR: USA

TRANSFUSION, (SEP 2001) Vol. 41, No. 9, Supp. [S], SOURCE:

pp. 13S-13S.

Publisher: AMER ASSOC BLOOD BANKS, 8101 GLENBROOK

RD, BETHESDA, MD 20814-2749 USA.

ISSN: 0041-1132. Conference; Journal DOCUMENT TYPE:

LANGUAGE: English

REFERENCE COUNT:

L23 ANSWER 11 OF 27 SCISEARCH COPYRIGHT 2002 ISI (R)

2001:818200 SCISEARCH ACCESSION NUMBER:

THE GENUINE ARTICLE: 472TV

Evidence for transmission of Babesia microti TITLE:

from Connecticut blood donors to recipients Cable R G (Reprint); Badon S; Trouem-Trend J;

AUTHOR: Militscher J E; Houghton R L; Lodes M

J; Persing D H; Eberhard M L; Pleniazek N J;

Herwaldt B L; Leiby D A

Amer Red Cross Blood Serv, Farmington, CT USA; Amer CORPORATE SOURCE:

Red Cross, Holland Lab, Rockville, MD USA; Corixa Corp, Seattle, WA USA; Ctr Dis Control & Prevent,

Atlanta, GA USA

COUNTRY OF AUTHOR: USA

TRANSFUSION, (SEP 2001) Vol. 41, No. 9, Supp. [S], SOURCE:

pp. 12S-13S.

Publisher: AMER ASSOC BLOOD BANKS, 8101 GLENBROOK

RD, BETHESDA, MD 20814-2749 USA.

ISSN: 0041-1132. Conference; Journal

DOCUMENT TYPE: LANGUAGE:

English

REFERENCE COUNT:

HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 6 L23 ANSWER 12 OF 27

ACCESSION NUMBER: 2000:725776 HCAPLUS

DOCUMENT NUMBER: 133:295360

TITLE: Antigens of Babesia microtia for use in the

diagnosis, prophylaxis, and treatment of

babesiosis

Reed, Steven G.; Lodes, Michael J.; Houghton, INVENTOR(S):

Raymond L.; Sleath, Paul R.;

Mcneill, Patricia D.

Corixa Corp., USA PATENT ASSIGNEE(S):

PCT Int. Appl., 118 pp. SOURCE:

CODEN: PIXXD2

DOCUMENT TYPE: Patent

English LANGUAGE:

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

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APPLICATION NO. DATE
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                             20001012
                                           WO 2000-US9136 20000405
     WO 2000060090
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             CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
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             RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
             US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
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                                           EP 2000-921771 20000405
     EP 1169455
                            20020109
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            AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
             PT, IE, SI, LT, LV, FI, RO
                       A1
                             20011011
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                                                              20001213
     US 2001029295
                                          US 1999-286488 A 19990405
PRIORITY APPLN. INFO.:
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                                                           A 20000317
                                          US 1996-723142
                                                           A2 19961001
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                                                           A2 19970424-
                                          US 1997-990571
                                                           A2 19971211
                                         WO 1998-US26437
                                                          A2 19981211
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                                          US 2000-656688
                                          US 2000-685436
                                                           A2 20001010
                          MARPAT 133:295360
OTHER SOURCE(S):
     Compds. and methods for the diagnosis and treatment of B. microtia
     infection are disclosed. The compds. provided include polypeptides
     that contain at least one antigenic portion of a B. microtia antigen
     and DNA sequences encoding such polypeptides. Antigenic epitopes of
     such antigens are also provided, together with pharmaceutical
     compns. and vaccines comprising such polypeptides, DNA sequences or
     antigenic epitopes. Diagnostic kits contg. such polypeptides, DNA
     sequences or antigenic epitopes and a suitable detection reagent may
     be used for the detection of B. microtia infection in patients and
     biol. samples. Antibodies directed against such polypeptides and
     antigenic epitopes are also provided. Cloning of antigen genes by
     antibody screening of expression libraries with antiserum.
     Seventeen antigens were identified and several of these showed
     common sequences. The clones also contained telomere repeat
     sequences indicating that they were located near the telomere. Use
     of the antigens in diagnostic detection of B. microtia is
     demonstrated.
                                THERE ARE 2 CITED REFERENCES AVAILABLE FOR
REFERENCE COUNT:
                          2
                                THIS RECORD. ALL CITATIONS AVAILABLE IN
                                THE RE FORMAT
                       WPIDS (C) 2002 THOMSON DERWENT
L23 ANSWER 13 OF 27
ACCESSION NUMBER:
                       2000-160675 [14]
                                          WPIDS
                       1998-609891 [51]; 2002-062250 [01]
CROSS REFERENCE:
                       N2000-119888
DOC. NO. NON-CPI:
DOC. NO. CPI:
                       C2000-050162
TITLE:
                       New compounds and methods for the diagnosis of
                       Ehrlichia infection, particularly Human
                       granulocytic ehrilichiosis.
```

DERWENT CLASS:

A96 B04 D16 S03

INVENTOR(S):

HOUGHTON, R L; LODES, M J; MCNEILL, P D; REED, S G

PATENT ASSIGNEE(S):

(CORI-N) CORIXA CORP; (HOUG-I) HOUGHTON R L;

(LODE-I) LODES M J; (MCNE-I) MCNEILL P D; (REED-I)

REED S G

85

COUNTRY COUNT:

PATENT INFORMATION:

PA'	rent	NO	KIND	DATE	WEEK	LA	PG	
WO	2000	00061	5 A2	20000106	(200014)*	EN	108	

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC

MW NL OA PT SD SE SL SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZA ZW

AU 9948474 A 20000117 (200026) US 6277381 B1 20010821 (200150) US 6306402 B1 20011023 (200165) EP 1144639 A2 20011017 (200169) EN

R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

US 2002064535 A1 20020530 (200240)

#### APPLICATION DETAILS:

PATENT NO KIND	)	APPLICATION	DATE
WO 2000000615 A2	:	WO 1999-US14793	19990629
AU 9948474 A		AU 1999-48474	19990629
US 6277381 B1	CIP of	US 1997-821324	19970321
	CIP of	US 1997-975762	19971120
	CIP of	US 1998-106582	19980629
	CIP of	US 1998-159469	19980923
		US 1999-295028	19990420
US 6306402 B1	CIP of	US 1997-821324	19970321
	CIP of	US 1997-975762	19971120
		US 1998-106582	19980629
EP 1144639 A2		EP 1999-932087	19990629
		WO 1999-US14793	19990629
US 2002064535 A1	CIP of	US 1997-821324	19970321
	CIP of	US 1997-975762	19971120
	Cont of	US 1998-106582	19980629
		US 1998-159469	19980923

#### FILING DETAILS:

PAT	ENT N	O K	IND		PAT	ENT NO
ΕP	99484 11446 20020	39	A2	Based on Based on CIP of CIP of	WO US	200000615 200000615 6207169 6231869
				Cont of	US	6306402

PRIORITY APPLN. INFO: US 1999-295028 19990420; US 1998-106582 19980629; US 1998-159469 19980923; US

Searcher :

Shears

308-4994

1997-821324 19970321; US 1997-975762 19971120

AN 2000-160675 [14] WPIDS

CR 1998-609891 [51]; 2002-062250 [01]

AB WO 200000615 A UPAB: 20020701

NOVELTY - A polypeptide (P) comprising an immunogenic portion of an Ehrlichiaantigen or its variant that is encoded by one of 18 DNA sequences of 201-7091 base pairs (bp) (I)-(XVIII) (all sequences fully defined in the specification), their complements and DNA sequences that hybridize to sequences (I)-(XVIII), are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for

the following:

- (1) An antigenic epitope (E) of an Ehrlichia antigen comprising an amino acid sequence of (XIX) or (XX) consisting of 41 and 125 amino acids (aa) respectively;
  - (2) A polypeptide (P') comprising at least two of (E);
- (3) A DNA molecule (N) comprising a nucleotide sequence encoding (P) or (P');
  - (4) A recombinant expression vector (V) comprising (N);

(5) A host cell (H) transformed with (N);

- (6) A fusion protein (F) comprising either at least one of (P) or (P') and/or at least one of (E) or a 376 aa sequence (XXI) and/or a 325 aa sequence (XXII).
- (7) detecting Ehrlichia infection, Lyme disease and Babesia microtiinfection in a patient comprising:
- (a) contacting a biological sample with at least one of (E), (P), (P') or (F) and a Lyme disease antigen and a B.microti antigen; and
- (b) detecting the presence of antibodies that bind to (E), (P), (P') or (F) or the Lyme disease antigen or the B.microti antigen in the sample;
  - (8) A method similar to (7), comprising:
- (a) contacting a biological sample with a specific binding agent to at least one of (E), (P), (P') or (F) or a Lyme disease antigen and a B.microti antigen; and
- (b) detecting a polypeptide that binds to the binding agent, thereby detecting Ehrlichiainfection;
  - (9) A method similar to (7), comprising:
- (a) contacting the sample with one or more probe oligonucleotides (or at least two primer oligonucleotides in a PCR reaction) where at least one is specific for (N); and
- (b) detecting in the sample a DNA sequence that hybridizes to (or amplifies in the presence of) the oligonucleotide primers, thereby detecting Ehrlichia infection;
  - (10) A diagnostic kit (K) comprising:
  - (a) at least one of (P), (P'), (E) or (F); and
  - (b) a detection agent;
- (11) A diagnostic kit (K') comprising at least two oligonucleotide primers or one oligonucleotide probe whereby at least one is specific for (N);
- (12) A monoclonal antibody or polyclonal antibody that binds to (P), (P') or (E); and
- (13) Vaccines comprising at least one of (P), (P'), (N) or (E) and a non-specific immune enhancer such as an adjuvant;
- (14) A polypeptide comrpising an immunogenic portion of an Erlichia antigen associated with human granulocytic erlichiosis or its variant.
  - All sequences are fully defined in the specification. USE (P), (P'), (N), (F) and/or (E) are useful for the

detection and treatment of Ehrlichiainfection. (P), (P'), (F) and/or (E) can also be used to detect Lyme disease and B.microtiinfection. In particular, (P') can be used for the serodiagnosis and treatment of human granulocytic ehrlichiosis (HGE). Compositions of (P) or (P'), (N) and (E) can be used in the manufacture of a medicament for inducing protective immunity in a patient. The new vaccines are also used for inducing protective immunity in a patient.

ADVANTAGE - None given.

Dwg.0/2

PUBLISHER:

L23 ANSWER 14 OF 27 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 7

2000:282570 HCAPLUS ACCESSION NUMBER:

133:72606 DOCUMENT NUMBER:

Serological expression cloning of novel TITLE:

immunoreactive antigens of Babesia

microti

Lodes, Michael J.; Houghton, AUTHOR(S):

Raymond L.; Bruinsma, Elizabeth S.;

Mohamath, Raodoh; Reynolds, Lisa D.; Benson, Darin R.; Krause, Peter J.; Reed, Steven

G.; Persing, David H.

Corixa Corporation, Seattle, WA, 98104, USA CORPORATE SOURCE:

Infection and Immunity (2000), 68(5), 2783-2790 SOURCE:

CODEN: INFIBR; ISSN: 0019-9567 American Society for Microbiology

Journal DOCUMENT TYPE: English

LANGUAGE: Increased recognition of the prevalence of human babesiosis in the United States, together with rising concern about the potential for transmission of this infection by blood transfusion, has provided motivation to develop definitive serol. and mol. tests for the causative agent, Babesia microti. To develop more sensitive and specific assays for B. microti, the authors screened a genomic expression library with patient serum pools. This screening resulted in the identification of three classes of novel genes and an addnl. two novel, unrelated genes, which together encode a total of 17 unique B. microti antigens. The first class (BMN1-2 family) of genes encodes seven closely related antigens with a degenerate six-amino-acid repeat that shows limited homol. to Plasmodium sp. merozoite and sporozoite surface antigens. A second class (BMN1-8 family) of genes encodes six related antigens, and the third class (BMN1-17 family) of genes encodes two related antigens. The two remaining genes code for novel and unrelated sequences. Among the three classes of antigens and remaining novel sequences, five were chosen to code for the most immunodominant antigens (BMN1-2, -9, -15, and -17 and MN-10). Western blot anal. with the resulting recombinant proteins indicated that these antigens were targets of humoral immune responses during B. microti infection in humans.

REFERENCE COUNT: THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

MEDLINE DUPLICATE 8 L23 ANSWER 15 OF 27

ACCESSION NUMBER: 2000344709 MEDLINE

20344709 PubMed ID: 10885987 DOCUMENT NUMBER:

TITLE: Babesiosis.

AUTHOR: Homer M J; Aquilar-Delfin I; Telford S R

3rd; Krause P J; Persing D H

CORPORATE SOURCE: Corixa Corporation and The Infectious Disease

Research Institute, Seattle, Washington 98104, USA.

SOURCE: CLINICAL MICROBIOLOGY REVIEWS, (2000 Jul) 13 (3)

451-69. Ref: 245

Journal code: 8807282. ISSN: 0893-8512.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200008

ENTRY DATE: Entered STN: 20000811

Last Updated on STN: 20000811 Entered Medline: 20000803

Babesiosis is an emerging, tick-transmitted, zoonotic disease caused AB by hematotropic parasites of the genus Babesial Babesial parasites (and those of the closely related genus Theileria) are some of the most ubiquitous and widespread blood parasites in the world, second only to the trypanosomes, and consequently have considerable worldwide economic, medical, and veterinary impact. The parasites are intraerythrocytic and are commonly called piroplasms due to the pear-shaped forms found within infected red blood cells. The piroplasms are transmitted by ixodid ticks and are capable of infecting a wide variety of vertebrate hosts which are competent in maintaining the transmission cycle. Studies involving animal hosts other than humans have contributed significantly to our understanding of the disease process, including possible pathogenic mechanisms of the parasite and immunological responses of the host. To date, there are several species of Babesia that can infect humans, Babesia microti being the most prevalent. Infections with Babesia species generally follow regional distributions; cases in the United States are caused primarily by B. microti, whereas cases in Europe are usually caused by Babesia divergens. The spectrum of disease manifestation is broad, ranging from a silent infection to a fulminant, malaria-like disease, resulting in severe hemolysis and occasionally in death. Recent advances have resulted in the development of several diagnostic tests which have increased the level of sensitivity in detection, thereby facilitating diagnosis, expediting appropriate patient management, and resulting in a more accurate epidemiological description.

L23 ANSWER 16 OF 27 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 9

ACCESSION NUMBER: 2000:74595 HCAPLUS

DOCUMENT NUMBER: 133:100272

TITLE: A polymorphic multigene family encoding an

immunodominant protein from Babesia

microti

AUTHOR(S): Homer, M. J.; Bruinsma, E. S.;

Lodes, M. J.; Moro, M. H.; Telford, S.,

III; Krause, P. J.; Reynolds, L. D.; Mohamath,

R.; Benson, D. R.; Houghton, R. L.;

Reed, S. G.; Persing, D. H.

CORPORATE SOURCE: Department of Laboratory Medicine and Pathology,

Mayo Clinic, Rochester, MN, 55905, USA

SOURCE: Journal of Clinical Microbiology (2000), 38(1),

362-368

CODEN: JCMIDW; ISSN: 0095-1137
American Society for Microbiology

PUBLISHER: American
DOCUMENT TYPE: Journal
LANGUAGE: English

Human babesiosis in the United States is caused predominantly by AΒ Babesia microti, a tick-transmitted blood parasite. Improved testing methods for the detection of infection with this parasite are needed, since asymptomatic B. microti infection represents a potential threat to the blood supply in areas where B. microti is endemic. We performed immunoscreening of an expression library of genomic DNA from a human isolate of B. microti (strain MN1). Among 17 unique immunoreactive clones, we identified 9 which represent a related family of genes with little sequence homol. to other known sequences but with an architecture resembling that of several surface proteins of Plasmodium. Within this family, a tandem array of a degenerate six-amino-acid repeat (SEAGGP, SEAGWP, SGTGWP, SGTVGP) was found in various lengths between relatively well conserved segments at the N and C termini. In order to examine within-clone variation, we developed a PCR protocol for direct recovery of a specific bmn1-6 homolog directly from 30 human blood isolates, 4 corresponding hamster isolates, and 5 geog. corresponding Peromyscus leucopus (white-footed mouse) isolates. Isolates from the hamsters had the same sequences as those found in the corresponding human blood, suggesting that genetic variation of bmn1-6 does not occur during passage. However, clones from different patients were often substantially different from each other with regard to the no. and location of the degenerate repeats within the bmn1-6 homolog. Moreover, we found that strains that were closely related geog. were also closely related at the sequence level; nine patients, all from Nantucket Island, Mass., harbored clones that were indistinguishable from each other but that were distinct from those found in other northeastern or upper midwestern strains. We conclude that considerable genetic and antigenic diversity exists among isolates of B. microti from the United States and that geog. clustering of subtypes may exist. The nature of the bmn1-6 gene family suggests a mechanism of antigenic variation in B. microti that may occur by recombination, differential

expression, or a combination of both mechanisms.

REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L23 ANSWER 17 OF 27 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 10

ACCESSION NUMBER: 2000:87236 HCAPLUS

DOCUMENT NUMBER: 133:57223

TITLE: Multiepitope synthetic peptide and recombinant

protein for the detection of antibodies to Trypanosoma cruzi in patients with treated or

untreated Chagas' disease

AUTHOR(S): Houghton, Raymond L.; Benson, Darin R.;

Reynolds, Lisa; McNeill, Patricia; Sleath, Paul; Lodes, Michael; Skeiky,

Yasir A. W.; Badaro, Roberto; Krettli, Antoniana

U.; Reed, Steven G.

CORPORATE SOURCE: Corixa Corporation, Seattle, WA, 98104, USA SOURCE: Journal of Infectious Diseases (2000), 181(1),

.

325-330

CODEN: JIDIAQ; ISSN: 0022-1899 University of Chicago Press

PUBLISHER: DOCUMENT TYPE: Journal English LANGUAGE:

A tetrapeptide and a recombinant protein, each representing 4 AB immunodominant epitopes of Trypanosoma cruzi, were tested by use of ELISA for the detection of serum antibodies. Sera from individuals with Chagas' disease, including persons untreated and successfully or unsuccessfully treated, were tested. These assays detected antibody in 100% of the parasitemias. The antibody reactivity decreased based on the success of treatment. Higher sensitivity was obsd. for tetrapeptide/recombinant protein assays than for lysate-based ELISA, and specificity was improved, particularly with Leishmania sera. The results indicate that multiepitope antigens provide a more sensitive and specific alternative to lysate for detection of anti-T. cruzi antibodies, as required for developing

blood screening assays. REFERENCE COUNT:

29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

L23 ANSWER 18 OF 27 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2000:394239 BIOSIS PREV200000394239 DOCUMENT NUMBER:

Characterization of the Babesia microti TITLE:

chronic carrier state in a murine model. Homer, M. J. (1); Bruinsma, E. S. (1); AUTHOR(S):

Aguilar-Delfin, I. (1); Moro, M. J. (1); Persing, D.

Η.

CORPORATE SOURCE:

SOURCE:

(1) Mayo Fndn, Rochester, MN USA

Abstracts of the General Meeting of the American Society for Microbiology, (2000) Vol. 100, pp. 283.

print.

Meeting Info.: 100th General Meeting of the American Society for Microbiology Los Angeles, California, USA May 21-25, 2000 American Society for Microbiology

. ISSN: 1060-2011.

DOCUMENT TYPE:

Conference English LANGUAGE: SUMMARY LANGUAGE: English

L23 ANSWER 19 OF 27 SCISEARCH COPYRIGHT 2002 ISI (R)

2000:888017 SCISEARCH ACCESSION NUMBER:

THE GENUINE ARTICLE: 364CN

Serologic and nucleic acid evidence for babesia TITLE:

microti in Connecticut (CT) blood donors

Leiby D A (Reprint); Chung A P; Triano L R; Cable R AUTHOR:

G; Houghton R L; Lodes M J

CORPORATE SOURCE: AMER RED CROSS, FARMINGTON, CT; CORIXA CORP,

SEATTLE, WA; AMER RED CROSS, ROCKVILLE, MD

COUNTRY OF AUTHOR: USA

TRANSFUSION, (OCT 2000) Vol. 40, No. 10, Supp. [S], SOURCE:

pp. S2-S2.

Publisher: AMER ASSOC BLOOD BANKS, 8101 GLENBROOK

RD, BETHESDA, MD 20814-2749.

ISSN: 0041-1132.

DOCUMENT TYPE: Conference; Journal

> Shears 308-4994 Searcher :

FILE SEGMENT:

LIFE; CLIN

LANGUAGE:

English

REFERENCE COUNT:

0

L23 ANSWER 20 OF 27 HCAPLUS COPYRIGHT 2002 ACS

DUPLICATE 11

ACCESSION NUMBER: DOCUMENT NUMBER:

1999:388301 HCAPLUS 131:85409

TITLE:

Antigen and gene sequences for diagnosis and

treatment of Babesia microti infection

INVENTOR(S):

Reed, Steven G.; Lodes, Michael

J.; Houghton, Raymond;

Sleath, Paul R.; Persing, David;

Bruinsma, Elizabeth

PATENT ASSIGNEE(S):

Corixa Corporation, USA; Mayo Foundation for

Medical Education and Research

SOURCE:

PCT Int. Appl., 126 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

	PAT	rent 1	NO.		KII	D	DATE				APF	DATE	DATE					
	WO	9929	A: JP,			0617			WO	199	8-U	S264	37	1998				
								DK.	ES.	F	[. F	R.	GB.	GR.	IE.	IT,	LU.	MC.
		1011.		PT,		01,	22,	<i>D</i> 10,	,		-, -	,	,	<b></b> ,	,	,	,	,
	US	6214	•	•		1	2001	0410			US	199	7-9	9057	L	1997	1211	
		9918					19990	0628			ΑU	199	9-1	8204		1998	1211	
		2001					2001	1011			US	200	0-7	37178	3	2000	1213	
PRIO		APP:								US	199	97-9	905	71	Α	1997	1211	
										US	199	96-7	231	42	Α2	1996	1001	
										US	199	97-8	452	58	Α2	1997	0424	
										WO	199	98-C	IS26	437	W	1998	1211	
										US	199	9-2	864	88	Α2	1999	0405	
										US	200	0-5	287	84	A2	2000	0317	
										WO	200	)0-U	IS91	36	A2	2000	0405	
										US	200	00-5	690	98	A2	2000	0510	
										US	200	00-6	057	24	Α2	2000	0627	
										US	200	00-6	566	88	A2	2000	0907	
										US	200	0-6	854	36	Α2	2000	1010	
ΔR	Con	nnds	and	meth	ahor	for	the	dia	nos	is	and	d tr	eati	ment	of	Babe	sia	

Compds. and methods for the diagnosis and treatment of Babesia microti infection are disclosed. The compds. provided include polypeptides that contain at least one antigenic portion of a B. microti antigen and DNA sequences encoding such polypeptides. Nine antigens share some homol., contain a degenerate repeat of six amino acids with 9-22 repeats occurring in each antigen, and bear some similarity to a Plasmodium falciparum merozoite surface antigen gene. A second group of five antigens bear some homol. to each other but do not show homol. to any previously identified sequences. Two synthetic peptides (BABS-1 and BABS-4) were made to the repeat region of isolated B. microti antigen BMNI-3. Twelve BMNI-6 homologs were obtained from hamster and human patients. Antigenic epitopes of such antigens are also provided, together with pharmaceutical compns. and vaccines comprising such polypeptides, DNA sequences or antigenic epitopes. Diagnostic kits contg. such polypeptides, DNA

sequences or antigenic epitopes and a suitable detection reagent may be used for the detection of B. microti infection in patients and biol. samples. Antibodies directed against such

polypeptides and antigenic epitopes are also provided.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN

THE RE FORMAT

L23 ANSWER 21 OF 27 MEDLINE DUPLICATE 12

ACCESSION NUMBER: 1999221786 MEDLINE

DOCUMENT NUMBER: 99221786 PubMed ID: 10203519

DOCUMENT NUMBER: 99221786 Pubmed ID: 10203519

TITLE: Detection of enzootic babesiosis in baboons (Papio cynocephalus) and phylogenetic evidence supporting

synonymy of the genera Entopolypoides and Babesia.

AUTHOR: Bronsdon M A; Homer M J; Magera J M;

Harrison C; Andrews R G; Bielitzki J T; Emerson C L;

Persing D H; Fritsche T R

CORPORATE SOURCE: Regional Primate Research Center, University of

Washington School of Medicine, Seattle, Washington

98195, USA.

CONTRACT NUMBER: AI35191 (NIAID)

AI41103-01 (NIAID)

RR00166 (NCRR)

SOURCE: JOURNAL OF CLINICAL MICROBIOLOGY, (1999 May) 37 (5)

1548-53.

Journal code: 7505564. ISSN: 0095-1137.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals OTHER SOURCE: GENBANK-AF081465

ENTRY MONTH: 199905

ENTRY DATE: Entered STN: 19990525

Last Updated on STN: 20000303 Entered Medline: 19990507

Blood smear evaluation of two baboons (Papio cynocephalus) AΒ experiencing acute hemolytic crises following experimental stem cell transplantation revealed numerous intraerythrocytic organisms typical of the genus Babesia. Both animals had received whole-blood transfusions from two baboon donors, one of which was subsequently found to display rare trophozoites of Entopolypoides macaci. An investigation was then undertaken to determine the prevalence of hematozoa in baboons held in our primate colony and to determine the relationship, if any, between the involved species. Analysis of thick and thin blood films from 65 healthy baboons (23 originating from our breeding facility, 26 originating from an out-of-state breeding facility, and 16 imported from Africa) for hematozoa revealed rare E. macaci parasites in 31%, with respective prevalences of 39, 35, and 12%. Phylogenetic analysis of nuclear small-subunit rRNA gene sequences amplified from peripheral blood of a baboon chronically infected with E. macaci demonstrated this parasite to be most closely related to Babesia microti (97.9% sequence similarity); sera from infected animals did not react in indirect fluorescent-antibody tests with Babesia microti antigen, however, suggesting that they represent different species. These results support an emerging view that the genus Entopolypoides Mayer 1933 is synonymous with that of the genus Babesia Starcovici 1893 and that the morphological variation noted

among intracellular forms is a function of alteration in host immune status. The presence of an underrecognized, but highly enzootic, Babesia sp. in baboons may result in substantial, unanticipated impact on research programs. The similarity of this parasite to the known human pathogen B. microti may also pose risks to humans undergoing xenotransplantation, mandating effective screening of donor animals.

L23 ANSWER 22 OF 27 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 13

ACCESSION NUMBER: 1999:316369 HCAPLUS

DOCUMENT NUMBER: 131:143166

TITLE: A multi-epitope synthetic peptide and

recombinant protein for the detection of

antibodies to Trypanosoma cruzi in radioimmunoprecipitation-confirmed and

consensus-positive sera

AUTHOR(S): Houghton, Raymond L.; Benson, Darin R.;

Reynolds Lisa D.: McNeill Patricia D

Reynolds, Lisa D.; McNeill, Patricia D.; Sleath, Paul R.; Lodes, Michael J.;

Skeiky, Yasir A. W.; Leiby, David A.; Badaro,

Roberto; Reed, Steven G.

CORPORATE SOURCE: Corixa Corporation, Seattle, WA, 98104, USA

SOURCE: Journal of Infectious Diseases (1999), 179(5),

1226-1234

CODEN: JIDIAQ; ISSN: 0022-1899

PUBLISHER: University of Chicago Press

DOCUMENT TYPE: Journal LANGUAGE: English

Peptide epitopes of Trypanosoma cruzi have been identified through expression cloning. A tripeptide (2/D/E) contg. three epitopes (TcD, TcE, PEP-2) was used in ELISA to detect antibodies to T. cruzi in 239 of 240 consensus-pos. sera and 41 of 42 sera confirmed pos. by radioimmunopptn. assay. The 1 discrepant consensus-pos. serum was used to expression-clone a novel gene that contained a repeat sequence. A peptide corresponding to this sequence, TcLo1.2, was specific for T. cruzi. This antigen detected the discrepant consensus-pos. serum and enhanced reactivity of low-pos. sera in the tripeptide assay. A branched synthetic peptide, 2/D/E/Lo1.2, or a linear recombinant, r2/D/E/Lo1.2, realized all of the diagnostic features of the 4 epitopes, including the ability to boost reactivity of low-reactive sera. Thus, peptides and recombinants contg. multiple repeat epitopes are powerful tools for developing assays for T. cruzi antibody detection and have direct application in blood screening.

REFERENCE COUNT:

41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L23 ANSWER 23 OF 27 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 14

ACCESSION NUMBER:

1998:229027 HCAPLUS

DOCUMENT NUMBER:

128:292989

TITLE:

Antigens of Babesia microtia and their use in

the diagnosis and treatment of infection

INVENTOR(S): Reed, Steven G.; Lodes, Michael

J.; Houghton, Raymond;

Sleath, Paul R.

PATENT ASSIGNEE(S):

Corixa Corp., USA

SOURCE:

Eur. Pat. Appl., 113 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

KIND DATE APPLICATION NO. DATE PATENT NO. -----\_\_\_\_ \_\_\_\_\_ \_\_\_\_\_ \_\_\_\_\_\_ EP 1997-117067 EP 834567 A2 19980408 19971001 A3 19990331 EP 834567 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI US 6306396 B1 20011023 US 1996-723142 19961001 US 1997-845258 US 6183976 B1 20010206 19970424 US 1996-723142 A 19961001 PRIORITY APPLN. INFO.: US 1997-845258 A 19970424

AB Antigens and epitopes of Babesia microti that can be used in the diagnosis and treatment of infection are described. Genes for the antigens or antibodies against them can be used in the detection of B. microti. CDNAS for these antigens were cloned by screening an expression library in .lambda.ZAP with antiserum to B. microti.

L23 ANSWER 24 OF 27 WPIDS (C) 2002 THOMSON DERWENT

ACCESSION NUMBER: 1998-609891 [51] WPIDS

CROSS REFERENCE: 2000-160675 [11]; 2002-062250 [01]

DOC. NO. CPI: C1998-182724

TITLE: Poly peptide(s) comprising immunogenic portion of

Ehrlichia antigen - and encoding DNA sequences,

useful for e.g. diagnosis and treatment of

Ehrlichia infection, especially human granulocytic

ehrlichiosis. A96 B04 D16

DERWENT CLASS: A96 B04 D16
INVENTOR(S): HOUGHTON, R; LODES, M J;

REED, S G; HOUGHTON, R L (CORI-N) CORIXA CORP

PATENT ASSIGNEE(S): (CORI-N) CO

COUNTRY COUNT: 81

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9842740 A2 19981001 (199851)\* EN 140

RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW

NL OA PT SD SE SZ UG ZW
W: AL AM AT AU BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB
GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU
LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ

TM TR TT UA UG UZ VN YU ZW

AU 9865794 A 19981020 (199909) EP 1007550 A2 20000614 (200033) EN

R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

US 6207169 B1 20010327 (200119)

US 6231869 B1 20010515 (200129)

JP 2002515763 W 20020528 (200238) 139

APPLICATION DETAILS:

PATENT NO KIND APPLICATION DATE

WO	9842740	A2			WO	1998-US5695	19980323
ΑU	9865794	Α			ΑU	1998-65794	19980323
ΕP	1007550	A2			EΡ	1998-911966	19980323
					WO	1998-US5695	19980323
US	6207169	В1	CIP	of .	US	1997-821324	19970321
					US	1997-975762	19971120
US	6231869	В1			US	1997-821324	19970321
JΡ	2002515763	W			JP	1998-545891	19980323
					WO	1998-US5695	19980323

#### FILING DETAILS:

PAT	TENT NO	KIND		PAT	PATENT NO							
AU	9865794	 А	Based	on	WO	9842740						
ΕP	1007550	A2	Based	on	WO	9842740						
JΡ	2002515763	3 W	Based	on	WO	9842740						

PRIORITY APPLN. INFO: US 1997-975762 19971120; US 1997-821324 19970321

AN 1998-609891 [51] WPIDS

CR 2000-160675 [11]; 2002-062250 [01]

AB WO 9842740 A UPAB: 20020701

A polypeptide comprising an immunogenic portion of an Ehrlichia antigen (or variant differing by conservative substitutions and/or modifications) is new, in which the antigen has amino acid sequence encoded by:

- (i) one of nineteen 201-7091 bp sequences given in the specification, encoding Ehrlichia antigens;
  - (ii) sequences hybridising to (i); or
  - (iii) complements of (i) or (ii).

Also claimed are:

- (1) an antigenic epitope of an Ehrlichia antigen with the 41 or 125 amino acid sequences (I) or (II) given in the specification, and a second polypeptide comprising at least two such antigenic epitopes.
  - (2) DNA molecules encoding polypeptides as above;
  - (3) expression vectors comprising (2);
- (4) host cells (e.g. E. coli, yeast or mammalian) transformed
  with (3);
- (5) fusion proteins comprising at least one of polypeptides and/or at least one of antigenic epitopes;
- (6) diagnostic kits comprising at least one polypeptide/antigenic epitope/fusion protein (optionally immobilised on solid support e.g. nitrocellulose) plus detection reagent (optionally comprising reporter group e.g. radioisotope conjugated to binding agent e.g. anti-immunoglobulin; and
- (7) monoclonal/polyclonal antibodies binding to polypeptides/antigenic epitope.
- USE The polypeptides are useful in the treatment of Ehrlichia infection, and as vaccines for the prevention of infection (claimed). They preferably comprise an immunogenic portion of an Ehrlichia antigen associated with human granulocytic ehrlichiosis (or a variant) (claimed) and are thus especially useful in the treatment of human granulocytic ehrlichiosis (HGE). The polypeptides, antigenic epitopes or DNA molecules can be combined with a suitable carrier in pharmaceutical compositions (claimed).

Such compositions and the vaccines of (7) are useful to manufacture medicaments for inducing protective immunity against Ehrlichia infection in patients (claimed), especially against HGE. The polypeptides/antigenic epitopes/fusion proteins are also useful to detect such infections in patients, by contacting biological samples (e.g. serum, and especially whole blood (claimed) with at least 1 polypeptide/antigenic epitope/fusion protein and detecting antibody binding (claimed). They can also be used to produce antibodies useful in diagnosis of such infections. The DNA molecules of (2) are similarly useful for diagnosing such infections (claimed). HGE is caused by a rodent bacterium normally transmitted to humans by the same tick which transmits Lyme disease and babesiosis. Co-infection with these diseases is thus possible, and the polypeptides/antigenic epitopes/fusion proteins may be used in methods to detect at least one of Ehrlichia infection, Lyme disease or B. microti infection in patients, by contacting samples (e.g. whole blood, saliva etc.) with at least one polypeptide/antigenic epitope/fusion protein, a Lyme disease antigen and a B. microti antigen, and detecting antibody binding (claimed); kits are provided (claimed). Dwg.0/2

L23 ANSWER 25 OF 27 CONFSCI COPYRIGHT 2002 CSA

ACCESSION NUMBER: 1998:37806 CONFSCI

DOCUMENT NUMBER: 98-037806

Immunoreactivity of recombinant antigens of Babesia TITLE:

microti isolated using serological expression

cloning

Houghton, R.L.; Bruinsma, E.S.; Moro, M.H.; AUTHOR:

Krause, P.J.; Reynolds, L.D.; Mohamath, R.; Benson,

D.R.; Lodes, M.J.; Reed, S.G.;

Persing, D.H.

CORPORATE SOURCE: Corixa Corporation, Seattle, WA, USA

ASTMH, 60 Revere Drive, Suite 500, Northbrook, IL SOURCE: 60062, USA, Abstracts available. Price \$10. Poster

Paper No. 558.

Meeting Info.: 981 5000: 46th Annual Meeting of the American Society of Tropical Medicine and Hygiene (9815000). Lake Buena Vista, FL (USA). 7-11 Dec 1997. American Society of Tropical Medicine and Hygiene.

DOCUMENT TYPE:

Conference

FILE SEGMENT:

AUTHOR:

English

DCCP LANGUAGE:

L23 ANSWER 26 OF 27 CONFSCI COPYRIGHT 2002 CSA

ACCESSION NUMBER: 2002:14683 CONFSCI

DOCUMENT NUMBER: 02-014683

Identification and partial characterization of TITLE:

secreted antigens from Babesia microti

using a novel approach Homer, M.J.; Lodes, M.J.;

Reynolds, L.D.; Houghton, R.L.; Persing,

CORPORATE SOURCE:

Corixa Corporation, Seattle, WA, USA

American Society for Tropical Medicine, 60 Revere SOURCE: Dr., Suite 500, Northbrook, IL 60062, USA; phone:

847-480-9592; fax: 847-480-9282; email:

astmh@astmh.org; URL: www.astmh.org. Poster Paper No.

671.

Meeting Info.: 000 5775: 50th Annual Meeting of the American Society for Tropical Medicine (0005775). Atlanta, GA (USA). 11-15 Nov 2001. Bill and Melinda Gates Foundation, Glaxo SmithKline, Oravax Inc.,

Berna Products.

DOCUMENT TYPE:

Conference

FILE SEGMENT:

DCCP

LANGUAGE:

English

L23 ANSWER 27 OF 27 CONFSCI COPYRIGHT 2002 CSA

ACCESSION NUMBER:

1998:37803 CONFSCI

DOCUMENT NUMBER:

98-037803

TITLE:

Geographic variation within a gene encoding an immunoreactive protein from Babesia **microti** 

AUTHOR:

Bruinsma, E.S.; Lodes, M.J.; Moro, M.;

Krause, P.J.; Reynolds, L.D.; Mohamath, R.; Benson,

D.R.; Houghton, R.L.; Reed, S.G.;

Persing, D.H.

CORPORATE SOURCE:

Dep. Med. and Pathol., Mayo Clinic, Rochester, MN,

USA

SOURCE:

ASTMH, 60 Revere Drive, Suite 500, Northbrook, IL 60062, USA, Abstracts available. Price \$10. Poster

Paper No. 554.

Meeting Info.: 981 5000: 46th Annual Meeting of the American Society of Tropical Medicine and Hygiene (9815000). Lake Buena Vista, FL (USA). 7-11 Dec 1997. American Society of Tropical Medicine and Hygiene.

DOCUMENT TYPE:

Conference

FILE SEGMENT:

DCCP

LANGUAGE:

English

FILE 'HOME' ENTERED AT 12:24:46 ON 30 AUG 2002

# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 30, 2002, 13:18:44 ; Search time 51.8 Seconds (without alignments) 12.866 Million cell updates/sec Run on:

BASK-853-CLAIM4 21 Title: Perfect score:

1 eagxxs 6 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

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×3# 747574 seqs, 111073796 residues

747574

Total number of hits satisfying chosen parameters: Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

A\_Geneseq\_032802: Database :

/ SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ф	Query Match L	90.5	90.5	90.5	90.5	90.5	90.5	90.5	90.5	90.5	90.5	0
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# ALIGNMENTS

AAW77585 standard; Protein; 47 AA (first entry) 30-OCT-1998 AAW77585; AAW77585

RESULT

Staphylococcus aureus protein of unknown function.

Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;

Staphylococcus aureus.

Misc-difference 1.47
Misc-difference 1.47
/note= "residues designated X are unspecified, and represented as Xaa in the specification" Location/Qualifiers

EP841394-A2

13-MAY-1998

97EP-0307485. 24-SEP-1997;

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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a Staphylococcus aureus protein of unknown function, and is encoded by a DNA sequence of the invention. The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, urinary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthealmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectent.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                             New nucleic acid sequences from Staphylococcus aureus WCHU29 - useful in vaccines and for treatment of bacterial infections of e.g.
                                                                 Knowles DJC;
Reichard RW, Rosenberg M;
                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 19; Length 47; Pred. No. 2.9e+02; Mismatches 2; Indels
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                                                                                                                                                                    respiratory tract and central nervous system
                                                                  Burnham MKR, Hodgson JE,
Nicholas RO, Pratt JM,
                                                                                                                                                                                       Claim 11; Page 267; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU61772 standard; Protein; 81 AA.
                               (SMIK ) SMITHKLINE BEECHAM CORP.
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          96US-0027032.
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
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the treatment, proteins and their associated DNA sequences are used in the treatment, prevention and diagnosts of medical conditions caused by pustulosis, hypertosis and osteonyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes proteins. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by once: The sequence data for this patent did not form part of the printed in the intention, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                               Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                              Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 81;
          Bhatia A;
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      SS,
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0; Mismatches
      Wang St
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                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID No 22967; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
      Mitcham JL, Wang
Jen S, Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU41551 standard; Protein; 97 AA.
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2000US-208841P.
2000US-216747P.
Persing DH, Mi
e J, Zhang Y,
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                                                                                                    2001-616774/71.
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Best Local Similarity
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                                                                                                                                  N-PSDB; AAS59620.
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02-JUN-2000;
07-JUL-2000;
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      Skeiky YAW,
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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving constituting a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clasorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponential diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human and approach of the printed invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central. nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 22; Length 10
Pred. No. 6.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes immunogenic protein #4138.
                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 58189; 103pp; English.
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2000US-208841P.
2000US-216747P.
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      Drmanac RT, Liu C,
                                                            2001-639362/73
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Best Local Similarity
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                                                                                          N-PSDB; AAS92017
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02-JUN-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and ostecomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a blinding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies opperative for a cares proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

C. Note: The sequence data for this patent did not form part of the printed presence of the contact of the printed presence of the contact of the printed presence of the printed pr
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                            Bhatia A;
                                                         Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID No 2746; 1069pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG27830 standard; Protein; 100 AA.
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23-AUG-2000; 2000US-0649167.
                                                   Persing DH, M.
e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                         treating acne vulgaris -
                                                                                                                                           WPI; 2001-616774/71.
N-PSDB; AAS59515.
(CORI-) CORIXA CORP.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 AA;
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                                                   Skeiky YAW,
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ABG27830 RESULT

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08-SEP-2000; 2000US-0232080
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14-SEP-2000; 2
14-SEP-2000; 2
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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08-SEP-2000;
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21-SEP-2000;
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26-SEP-2000;
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18-AUG-2000;
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08-SEP-2000;
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                                                                                                                                                                                                                          Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO syndrome (Synovitis, acne, contactions is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downrequlate expression and activity of P. acnes polypeptides and cherraining P. acnes proteins. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme immunosorbent assay (ELISA).

Configuration, but was obtained in electronic format directly from WIPPO CC at fitp.WiPpo.int/Pub/Published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.5%; Score 19; DB 22; Length 113; 66.7%; Pred. No. 6.9e+02; Indels iive 0; Mismatches 2; Indels
                               , Wang SS, Bhatia A;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen SEQ ID NO:11850.
                                                                                                                                                                                                 Example 1; SEQ ID No 4437; 1069pp; English.
                               Skeiky YAW, Persing DH, Mitcham JL,
L'maisonneuve J, Zhang Y, Jen S, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM84257 standard; Protein; 117 AA.
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2000US-0184664.
2000US-0186350.
2000US-0189874.
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                              WPI; 2001-616774/71.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 AA;
                                                                                              N-PSDB; AAS59520
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|eagtas 104
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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activity, and can be used in gene therapy and vaccine production. (I)

activity, and can be used in gene therapy and vaccine production. (I)

creatment of diseases may be used in the prevention, diagnosis and

treatment of diseases associated with inappropriate (I) expression. For

example, they may be used to treat disorders associated with decreased

expression by rectifying mutations or deletions in a patient's genome

that affect the activity of (I) by expressing inactive proteins or to

supplement the patients own production of (I). Additionally, (I)

polynucleotides may be used to produce the secreted (I), by inserting

to another acids into a host cell and culturing the cell to express the

protein. (I) proteins and polynucleotides may be used to prevent,

diagnose and treat immune/haematopoietic-related diseases, especially

cancers and cancer metastases of haematopoietic-derived cells. AAK64703

to AAK87694 represent human immune/haematopoietic antigen genomic

sequences from the present invention. AAK34942 to AAK84950 and AAM82169

represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel human nucleic acid (cDNA) sequences (A), that are highly expressed in uterine tumour tissue and which have anticancer and cytostatic activity. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine or are used (i) to identify agents suitable for treatment of uterine or dometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequences expressed in uterine cancer tissues, and derived polypeptides, for treatment of uterine and endometrial cancer and identification of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endometrium; human; tumour; cancer; anticancer; cytostatic; EST:
treatment; uterine; gene therapy; expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 22; Length 117;
Pred. No. 7.2e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human endometrium tumour EST encoded protein 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY59973 standard; Protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Page 288; 444pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                              90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98DE-1017948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98DE-1017948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-591957/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ41991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eagtas 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE19817948-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eagxxs 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY59973;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY59973
           QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 11850; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0246611.
2000US-0246613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      000US-0249210.
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2000US-0246610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483426/52.
N-PSDB; AAK57038.
  13-OCT-2000;
20-OCT-2000;
20-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
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Gaps

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(expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTS from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular itssue. AAXS9941-Y6032B represent protein fragments encoded by the human endometrium tumour cDNA library derived EST fragments represented in AAZ41981-Z42121.
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody that interacts with collagen binding domain of Staphylococcal cna gene product - useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This protein comprises Staphylococcus aureus collagen binding protein (CBP) epitope MI7, i.e. amino acids 151-297 of full-length CBP, plus a vector derived N-terminal peptide. Claimed 441, 849 and 1500 bp nucleic acid sequences (see AAT93436-38) respectively encode CBP epitopes MI7, MI3 and MB5 (see AAM91552-54) that confer protection against S. aureus infection. These nucleic acid sequences can be used in the recombinant production of the CBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collagen binding protein; ona gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRAMM; adhesin; vaccine; immunisation; diagnosis; therapy;
                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Symersky J;
                                                                                                                                                                                              Score 19; DB 20; Length 118;
Pred. No. 7.2e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "vector pQE30-derived peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sthanam N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen binding protein M17 epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13..159
/note= "epitope M17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 1..12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patti JM,
                                                                                                                                                                                                                                                                                                                                                                              AAW31552 standard; Protein; 159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 31; Page 114; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TEXA ) UNIV TEXAS A & M SYSTEM
                                                                                                                                                                                               90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          House-Pompeo K,
                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylcoccus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-008801/01.
                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT93436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UABR-) UAB RES
                                                                                                                                                                                                                                                                                             34 eagsas 39
                                                                                                                                                                                                                                                              1 eagxxs 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epitope M17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                             AAW31552;
                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hook M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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a part of the trench in the beta sheet" 89..92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a portion of this region forms the beta sheet"
                                                                                                                                                                                                        Gaps
epitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in screening, diagnostic and therapeutic applications including active and passive immunisation and methods for the prevention of bacterial colonisation in an animal such as a human. The CBP epitopes are also contemplated for use in the preparation of vaccines and as carrier proteins in vaccine formulations, as well as in the formulation of compositions for the prevention of S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                           Collagen-binding region; CNA19; Staphylococcus aureus infection; Staphylococcus epidermidis infection; vaccine; CNA protein; cross-reactive antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Beta strand a; this region forms a part
the trench in the beta sheet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Beta strand b; this region forms a part the trench in the beta sheet"
                                                                                                                                                                                                        ö
                                                                                                                                                                               Length 159;
                                                                                                                                                                  Score 19; DB 19; Length 12.
Pred. No. 9.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Beta strand h; a part of the trench in t 140..149
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157..167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Beta strand c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Alpha helix 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Beta strand g"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Beta strand j"
                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus CNA19 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Beta strand
                                                                                                                                                                                                                                                                                                               AAE11855 standard; Protein; 168 AA
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                                                                                                                                                                               90.5%;
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                        Conservative
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/note=
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                             159 AA;
                                                                                                                      aureus infection.
                                                                                                                                                                                                                                                    28 eagtss 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200170267-A1
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                                                                                                                                                                                                                                                                                                                                                             18-DEC-2001
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                       AAE11855;
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Region
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                                                                                                                                                                                                                                                                                       RESULT
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bask-853-claim4.rag

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The sequences given in AAR39712-13 represent varient neutral proteases based on the Aspergillus oryzae protease sequence (see also AAR39711).
                                                                                                                                                                                                                                                                      This sequence represents a wildtype protease which may be used as the basis for the production of a varient neutral protease. The varient protease has either Cys6 or Cys78 substituted with an amino acid which has no -SH group. The varient proteases (see also AAR39713-14) have lower thermal stability than the WT and may be used in soy fermantation microorganisms. Soy produced by these microorganisms may be made into food products which will not be degraded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wildtype; protease; varient; neutral; mercapto group; food products; thermal stability; soy fermantation.
                                                                                                                                           New variant neutral protease II - includes cysteine substd. with aminoacid having no mercapto gp. in aminoacid sequence of yellow green koji mould neutral protease II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New variant neutral protease II - includes cysteine substd. with aminoacid having no mercapto gp. in aminoacid sequence of yellow green koji mould neutral protease II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 14; Length 177;
Pred. No. 1.1e+03;
0; Mismatches 2; Indels
                                             (SHSA ) SHOKUHIN SANGYO KOSOKINO HENKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHSA ) SHOKUHIN SANGYO KOSOKINO HENKA
                                                                                                                                                                                                                                Disclosure; Page 7-8; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR39712 standard; Protein; 177 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A. oryzae C6A neutral protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91JP-0344443.
    91JP-0344443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          presence of protease.
                                                                                     WPI; 1993-247571/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-247571/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 AA;
                                                                                                        N-PSDB; AAQ46955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eagsts 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 eagxxs 6
26-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR39712
    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an antibody which recognises a collagen-binding region including CNA19 of CNA protein from Staphylococcus aureus. This artibody is cross-reactive to collagen binding region of both S. aureus and S. epidermidis. It is useful for preventing or treating S. aureus or S. epidermidis infection in human or animal, and for displacing S. aureus or S. epidermidis bound to collagen. Antibody of the invention is useful for interfering with, modulating, and inhibiting the binding interactions between Staphylococcal bacteria and collagen, for detecting the presence of Staphylococcal bacteria or Staphylococcal collagen or binding proteins, to diagnose Staphylococcal immunisation against Staphylococcal infections, as research tools, for development of vaccine for passive immunisation against Staphylococcal infections, and in production facilities or laboratories to isolate additional quantities of collagen-binding proteins. It is also useful for treating medical instruments in order to reduce or eliminate the possibility of them becoming infected or further spreading the infection. The present sequence is S. aureus CNA19 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                      Novel isolated antibody which recognizes collagen-binding peptide such as CNA19 peptide from Staphylococcus aureus, useful for preventing or treating Staphylococcus aureus or epidermidis infection
                                                                                                                                                                                                                                                      Patel P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wildtype; protease; varient; neutral; mercapto group; food products; thermal stability; soy fermantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                      Patti J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 22; Length 168;
Pred. No. 1e+03;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                    Casolini F,
                                                                                                                                                                                                                                                  Hook M, Xu Y, Speziale P, Visai L,
Domanski P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR39711 standard; Protein; 177 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 2A; 107pp; English.
                                                                                                                                                               (INHI-) INHIBITEX INC.
(TEXA ) UNIV TEXAS A & M SYSTEM.
(UYPA-) UNIV PAVIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. oryzae WT neutral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.58;
                                       19-MAR-2001; 2001WO-US08554.
                                                                                                    25-APR-2000; 2000US-199370P.
15-AUG-2000; 2000US-225402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91JP-0344443.
                                                                                2000US-189968P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                               WPI; 2001-607512/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||| |
16 eagtss 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP05168479-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eagxxs
27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR39711;
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RESULT 10 AAR39711

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AAB24437 standard; Protein; 207
                                                                                 (first entry)
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                                                                                                                                                                                                                              WO200035937-A1.
                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                          17-DEC-1998;
18-DEC-1998;
                                                                                                                                                                                                                                                                      16-DEC-1999;
                                                                                 20-NOV-2000
                                                                                                                                                                                                                                                  22-JUN-2000
                                                                                                                                                                                                                                                                                                                                             Ruben SM,
Duan DR,
                                                              AAB24437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                      13
                                AAB24437
                                                    ö
These varient proteases have either Cys6 or Cys78 substituted with an amino acid which has no -SH group. These varient proteases have lower thermal stability than the WT and may be used in soy fermantation microorganisms. Soy produced by these microorganisms may be made into food products which will not be degraded by the presence of protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                based on the Aspergillus oryzae protease sequence (see also AAR39711). These varient proteases have either Cys6 or Cys78 substituted with an amino acid which has no -SH group. These varient proteases have lower thermal stability than the WT and may be used in soy fermantation microorganisms. Soy produced by these microorganisms may be made into food products which will not be degraded by the presence of protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences given in AAR39712-13 represent varient neutral proteases
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                          Wildtype; protease; varient; neutral; mercapto group; food products;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New variant neutral protease II - includes cysteine substd. with aminoacid having no mercapto gp. in aminoacid sequence of yellow green koji mould neutral protease II
                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 14; Length 177;
Pred. No. 1.1e+03;
0; Mismatches 2; Indels
                                                                                           Length 177;
                                                                                                                Indels
                                                                                 Score 19; DB 14; L6
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SHSA ) SHOKUHIN SANGYO KOSOKINO HENKA
                                                                                                                                                                                                                                                                                                     thermal stability; soy fermantation.
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                          AAR39713 standard; Protein; 177 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 8; 9pp; Japanese.

    A. oryzae C78A neutral protease.

                                                                                                                0;
                                                                                           90.5%;
                                                                                                                                                                                                                                                                                                                                                               /label= C78A
                                                                                                                                                                                                                                                                                                                                                                                                                           91JP-0344443.
                                                                                                                                                                                                                                                  (first entry)
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-247571/31.
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                       Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                     Misc-difference 78
                                                             177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 AA;
                                                                                                                                                        eagsts 70
                                                                                                                                    1 eagxxs 6
                                                                                                                                                                                                                                                                                                                                                                                   JP05168479-A
                                                                                                                                                                                                                                                                                                                                                                                                                          26-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                              26-DEC-1991;
                                                                                                                                                                                                                                                 24-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-1993
                                                               Sequence
                                                                                                                                                                                                                              AAR39713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                     RESULT 12
                                                                                                                                                        65
                                                                                                                Matches
                                                                                                                                                                                                 AAR39713
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The polynucleotide sequence given in AAA78381 to AAA78432 encode the human secreted proteins given in AAB24437 to AAB24604. Human secreted proteins given in AAB24437 to AAB24604. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Examples of activities include: cytostatic; antianaemic; antidabetic; antinflammatory; ophthalmological; antirheumatic; antiarthritic; antiporiatic; antimicrobial and antiparkinsonian.

Thuman secreted protein polynucleotides, polypeptides, antagonists and/or agonists may be useful in treating, preventing, and/or diagnosing other disorders of the immune system; (c) angiogenesis disorders; (b) disorders of the immune system; (c) angiogenesis disorders; (d) hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases associated with increase apoptosis; (g) neurological diseases; and sociated with increase apoptosis; (g) neurological diseases; and hipercious diseases. They are also used to promote wound healing.

AAA78372 to AAA78380 and AAB24436 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful
                                                                                          Human; secreted protein; cytostatic; antianaemic; antidiabetic; antianfammatory; ophthalmological; antisheumatic; antiarthritic; antisportatic; antianglogenic; cardiant; anti-HIV; nootropic; neuroprotective; antimicrobial; antiparkinsonian; cancer; immune system disorder; angiogenesis; hyperproliferative disorder; cardiovascular disorder; apoptosis; neurological disease; infectious disease; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Forty seven human nucleic acids encoding secreted proteins, usefu
the treatment, prevention and diagnosis of cancers, disorders of
immune system, angiogenesis disorders, neurological diseases and
hyperproliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Endress GA, Soppet DR, Ni J;
Shi Y, Lafleur DW, Olsen HS, Florence K;
Human secreted protein sequence encoded by gene 1 SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 21; Length 20
Pred. No. 1.3e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 478-479; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0112809.
98US-0113006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US29950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ebner R,
Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-431566/37.
N-PSDB; AAA78381.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 eagxxs
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Gaps

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Conservative

eagsts 70

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eagxxs 6

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Query Match Best Local Similarity Matches 4; Conserv

90.5%;

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This protein comprises Staphylococcus aureus collagen binding protein (GBP) epitope M31, i.e. amino acids 61-343 of full-length comprises District Claimed 441, 849 and 1500 bp nucleic acid sequences (see AAT93436-38) respectively encode CBP epitopes M17, M31 and M55 (see AAT93436-38) respectively encode CBP epitopes M17, M31 and M55 (see AAT93436-38) respectively concern concerns and be used in the recombinant production of the CBP epitopes. The CBP protein and antigenic epitopes are contemplated for use in the treatment of pathological infections, especially to prevent bacterial adhesion to collagen. The claimed nucleic acids as well as claimed anti-CBP antibodies will also be of use in serion and methods for the prevention of bacterial colonisation in an animal such as a human. The CBP catches and as carrier proteins in vaccine formulations, as well as inthe formulation of compositions for the prevention of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody that interacts with collagen binding domain of Staphylococcal cna gene product – useful to prevent bacterial sepsis in animal infected with Staphylococcus aureus
                                                                                                                                                   Collagen binding protein; ona gene; sepsis; infection; microbial surface component regonising adhesive matrix molecule; MSCRAMM; adhesin; vaccine; immunisation; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sthanam N, Symersky J;
                                                                                                                                                                                                                                                                                         /note= "vector pQE30-derived peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 31; Page 115-116; 143pp; English.
                                                                                                                         Collagen binding protein M31 epitope.
                                                                                                                                                                                                                                                                                                            13..211
/note= "epitope M31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patti JM,
                                                                                                                                                                                                                                                               Location/Qualifiers
                             AAW31553 standard; Protein; 211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UABR-) UAB RES FOUND.
(TEXA ) UNIV TEXAS A & M SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US08210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0017678.
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hook M, House-Pompeo K,
                                                                                                                                                                                                                                  Staphylcoccus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-008801/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT93437.
                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                         WO9743314-A2
                                                                                          21-MAY-1998
                                                                                                                                                                                                   epitope M31
                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                           AAW31553;
                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                            Protein
RESULT 14
              AAW31553
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Gaps

; 0

90.5%; Score 19; DB 19; Length 211; 66.7%; Pred. No. 1.3e+03; 1ve 0; Mismatches 2; Indels

Best\_Local Similarity 66.7 Matches 4; Conservative

Query Match

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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The case and so used in diagnostics as expressed sequence tags to restore normal activity of (II) is useful in gene therapy techniques (C restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical inspirators involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity amino acid sequences. Abg00010-Abg30377 represent novel human and amino acid sequences. Abg0010-Abg30377 represent novel human and mannary and and approaches of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic. food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 22; Length 225;
Pred. No. 1.4e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 33410; 103pp; English.
                                                                                                                                                                                                                                                 Novel human diagnostic protein #3042.
                                                                                                                                ABG03051 standard; Protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                           13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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N-PSDB; AAS67238.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                    40200175067-A2.
                                  34 eagtss 39
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1 eagxxs 6
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                         ABG03051;
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990S-0139456.
990S-0139457.
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990S-0139461.
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990S-014508.
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990S-014538.
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990S-0147333.
99US-0139455
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23 - 70x - 1999;

23 - 70x - 1999;

23 - 70x - 1999;

24 - 70x - 1999;

25 - 70x - 1999;

26 - 70x - 1999;

27 - 70x - 1999;

28 - 70x - 1999;

29 - 70x - 1999;

20 - 70x - 1
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05-AUG-1999;
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04-AUG-1999
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16-AUG-1999
                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 1356.
                                                                                           AA.
                                                                                        AAG05085 standard; Protein; 229
                                                                                                                                                                                                                                                                                                                                                                                                       990S-0121825.
990S-0123180.
990S-0125788.
990S-0125788.
990S-0126785.
990S-0126785.
990S-0126785.
990S-0128714.
990S-0128714.
990S-0130871.
990S-0130871.
990S-0132486.
990S-0132486.
990S-0132486.
990S-0134286.
990S-0134218.
                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000; 2000EP-0301439
                                                                                                                                                      17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                               Arabidopsis thaliana
           eagtss 21
                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
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19-APR-1999;
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23-APR-1999;
30-APR-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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28-MAY-1999;
01-JUN-1999;
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10-JUN-1999;
14-JUN-1999;
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17-JUN-1999;
18-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               666
                                                                                                                       AAG05085;
                                                          RESULT 16
             16
                                                                           AAG05085
             QQ
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AAM2563. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiants. inflammatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiandemic; antiadementic; uninerary; antibactic; observable; dermatological; antialengenic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; of inflammaticial and polynucleotides are useful for screening for apondatis of antidaponists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation; rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombooytopaenia, wounds, burns, ulcers, cateniniis, asthma, diabetes, cancer, multiple sclerosis, depression, all all and disorders.

Alzhehmer's disease, Parkinson's disease, neurodegenerative and envological disorders.
                                                                                                                                                antibrilarmatory; antirheumatic; antiarthritic; immunosuppressive; antibracterial; endocrine; cardiant; central nervous system; virucide; antibracterial; endocrine; cardiant; central nervous system; virucide; anti-HTV; fungicalde; antimutagen; cardiovascular; antianaemic; anamia; ecramic dermatopogical; antialergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidapersesant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; panoreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                  Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                  Human protein sequence SEQ ID NO:987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 207; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-DEC-2000; 2000WO-US35017,
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              neurological disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                             16-OCT-2001
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                          AAM25472;
         Score 19; DB 21; Length 229;
Pred. No. 1.4e+03;
0; Mismatches 2; Indels
990S-0149175.
990S-0149723.
990S-0149723.
990S-0149723.
990S-0149929.
990S-0149902.
990S-0149902.
990S-0150884.
990S-0151086.
990S-0151086.
990S-0151086.
990S-0151089.
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990S-0157865.
990S-0158029.
990S-01583369.
990S-0159293.
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99US-0155139.
99US-0155486.
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99US-0159330.
99US-0159331.
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66.7%;
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99US-0157117
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99US-0159638
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99US-0160767
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Matches 4; Conserv
                                                                                                           23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
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24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
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05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
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14-0CT-1999;
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21-0CT-1999;
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25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
                                                                                          23-AUG-1999
                                                                                                                                                                                                                                                                             07-SEP-1999
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20-SEP-1999
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13-OCT-1999
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14-OCT-1999
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18-OCT-1999
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25-OCT-1999
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Gaps

; 0

4; Conservative

g ò

AAM25472 ID AAM25472 standard; Protein; 242 AA.

RESULT 17

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9905 - 0.139453

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02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
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28-JUN-1999;
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02-JUL-1999;
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                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
              Gaps
           0;
             Indels
                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 1355.
     Pred. No. 1.5e+03;
; Mismatches 2;
                                                                                 AAG05084 standard; Protein; 243 AA
66.7%; Pre-
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                                                                                                                17-OCT-2000 (first entry)
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Matches 4; Conservative
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                           1 eagxxs 6
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06 - APR - 1999
06 - APR - 1999
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06-MAY-1999;
06-MAY-1999;
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-MAY-1999;
-MAY-1999;
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                                                                                                 AAG05084;
                                                                          AAG05084
                            ŏ
                                          Db
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SOC-2/CRAC-1; calcium channel; human; store operated channel; calcium release activated channel; therapy; diagnosis; lymphocyte proliferative disorder.

Human calcium channel SOC-2/CRAC-1.

10-OCT-2000

AAY95431;

AAY95431 standard; Protein; 243 AA.

19

AAY95431

'note= "encoded by SCA"

Location/Qualifiers 103

Key Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference

Homo sapiens.

by CSA"

"encoded

/note=

'note= "encoded by RSC"

by GNT"

'note= "encoded

/note= "encoded by NCA"

WO200040614-A2

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Score 19; DB 21; Length 243;
Pred. No. 1.5e+03;
0; Mismatches 2; Indels
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99US-0152363.
99US-0153070.
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99US-0156596.
99US-0157117.
99US-0157753.
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99US-0160815.
99US-0160980.
99US-0160981.
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99US-0161992.
99US-0161993.
99US-0162142.
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99US-0151438
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99US-0154018
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99US-0155139
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99US-0159638
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99US-0160770
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99US-0161404
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99US-0161361
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Best Local Similarity
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20-AUG-1999
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23-AUG-1999
23-AUG-1999
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25-AUG-1999
27-AUG-1999
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15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
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27 · OCT - 1999
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28-0CT-1999
28-0CT-1999
                                                                                                                                                                        27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
                                                                                                                                                                                                            31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
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(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

Scharenberg AM;

99US-0120018. 98US-0114220

29-JAN-1999; 22-JUN-1999; 30-DEC-1998;

99WO-US29996.

20-DEC-1999;

13-JUL-2000

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The present sequence is that of a partial sequence of human SOC-2/CRAC-1 (full-length sequence given in AAY95435), as deduced from a partial cDNA clone (see AAA4918). SOC-2/CRAC-1 is a member of a novel family of store operated channel (SOC) or calcium release activated channel (CRAC) polypeptides that modulate Ca2+ flux into and out of a cell, and which may be activated upon depletion of a cell, and which may be activated upon depletion of a cell. SOC-2/CRAC-1 is expressed predominantly in human hamanatopicitic cells, liver, spleen, heart and kidney.

Compositions for expressing functional SOC/CRAC calcium channel polypeptides in cells are expected to be useful for treating patients that have reduced extracellular calcium influx into their polypeptides in cells are expected to such cells to modulate therapeutic and/or imaging agents to such cells to modulate colleration and growth. SOC/CRAC polypeptides also represent traces for designing and/or identifying inhibitors that block lymphocyte proliferation and binding agents that selectively bind to SOC/CRAC polypeptides to which drugs or toxins can be conjugated to SOC/CRAC expressing cells. Methods for determining the level of SOC/CRAC expressing cells. Methods for determining the level of soc/CRAC expressing in a subject can be used to assess the presence, or absence, or stage of a proliferative disorder,
                                                                                                                                                                                                                                diagnose and treat proliferative disorders associated with the channel, and to screen for novel modulators of the channel
                                                                                                                                                                                New SOC/CRAC calcium channel polynucleotides and polypeptides used to
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page 58-59; 108pp; English
WPI; 2000-465957/40.
N-PSDB; AAA49918.
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Gaps

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Conservative

Matches

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eagxxs

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990S-0137502-990S-0137724-990S-01387724-990S-01387724-990S-0138847-990S-0139453-990S-0139453-990S-0139453-990S-0139455-990S-0139455-990S-0139455-990S-0139455-990S-0139457-990S-0142920-990S-0144332-990S-0144332-990S-0144332-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0144333-990S-0145088-990S-0145088-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145089-990S-0145088-990S-0145089-990S-0145089-990S-0145088-990S-0145089-990S-0145088-990S-0145089-990S-0145088-990S-0145089-990S-0145088-990S-0145089-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990S-0145088-990
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99US-0145224.
99US-0145276.
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99US-0145919.
99US-0145951.
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99US-0147302.
99US-0147192.
99US-0147260.
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04 - JUN - 1999)

07 - JUN - 1999)

10 - JUN - 1999)

11 - JUN - 1999)

14 - JUN - 1999)

16 - JUN - 1999)

17 - JUN - 1999)

18 - JUN - 1999)
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                                                                                                                   Gaps
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0
                                                                                 Score 19; DB 21; Length 243;
Pred. No. 1.5e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 1354.
   e.g. a lymphocyte proliferative disorder.
                                                                                                                                                                                                                                                                  AAG05083 standard; Protein; 257 AA.
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990S-0123180.
990S-01235180.
990S-0125788.
990S-0126785.
990S-0127462.
990S-0127462.
990S-0129813.
990S-0129814.
990S-0130077.
990S-0132486.
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990S-0132486.
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990S-0134370.
990S-0134768.
990S-0134941.
990S-0135353.
                                                                                 Query Match 90.5%;
Best Local Similarity 66.7%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                    243 AA;
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53 eagsss 58
                                                                                                                                                    1 eagxxs 6
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                                    Sequence
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Gaps

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Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J, Xu C,
Yang Y, Zaho QA, Chen R, Wang D, Goodrich RW, Liu C, Drmanac RT;
                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; antinflammatory; stem cell growth factor; activin; inhibin; cancer; nervous system disease; neuropathy, Alzheimer's disease;
Parkinson's disease; huntington's disease; spinal cord disorder;
Parkinson's disease; Huntington's disease; spinal cord disorder;
Parkinson's disease; Huntington's disease; spinal cord disorder;
platelet disorder; thrombocytopaenia; stem cell disorder;
platelet disorder; thrombocytopaenia; stem cell disorder;
psteoporosis; osteoarthritis; bone degenerative disorder;
periodontal disease; fibrosis; reperfusion; immune disorder;
severe combined immunodeficiency; infection; autoimmune disorder;
severe combined immunodeficiency; infection; autoimmune disorder;
sachma; coaqulation disorder; haemophilia; sepsis; nephritis;
inflammatory bowel disease; food supplement; immunogen.
                                                                                                                                                 Human novel cytokine encoded by cDNA 790CIP2D_8 #2.
  Mismatches
                                                                                     AAU68590 standard; Protein; 264 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 328; 336pp; English.
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2000US-0695618.
2000US-0728711.
2000US-0728711.
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2000US-0649167
                                                                                                                             16-JAN-2002 (first entry)
  Conservative
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N-PSDB; AAS59882.
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                                      184 eagsss 189
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                   1 eagxxs 6
                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                   RESULT 21
 Matches
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990S-0159295.
990S-0159329.
990S-0159331.
990S-0159637.
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990S-0160981.
990S-0161404.
990S-0161405.
990S-0161405.
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99US-0153070.
99US-0153758.
99US-0154018.
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99US-0154779.
99US-0155139.
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99US-0155659.
99US-0156458.
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99US-0157753.
99US-0157865.
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99US-0158232.
99US-0158369.
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99US-0160741.
99US-0160767.
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99US-0160814.
99US-0160815.
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990S-0161361.
990S-0161920.
990S-0161992.
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                                      99US-0148171
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99US-0151065
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01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
16-SEP-1999;
                                    10-AUG-1999;
11-AUG-1999;
12-AUG-1999;
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25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
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27-AUG-1999;
30-AUG-1999;
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22-SEP-1999;
23-SEP-1999;
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28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
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12-OCT-1999;
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14-0CT-1999;
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14-OCT-1999;
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1-0CT-1999;
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                                                                   13-AUG-1999
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17-AUG-1999
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20-AUG-1999
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06-0CT-1999
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26-OCT-1999
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The invention relates to isolated human polypeptides (which may be cytokines) and the polynucleotides encoding them. The protein is useful for identifying a compound which binds to it (e.g. modulators, agonists and antagonists). The polynucleotides are useful as an array for mismatch detection. The proteins and nucleic acids are useful as nutritional sources or supplements. The protein exhibits exhibits activity relating to cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity, immune stimulating or immune suppressing and activin or inhibin related activities. The proteins (and antibodies raised against them) and nucleic acids are therefore useful in the diagnosis and treatment of diseases and disorders such as cancer, central and peripheral nervous system diseases and neuropathies, Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic New polypeptides and nucleic acids, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone degenerative disorders, cancer and promoting wound healing

Score 19; DB 21; Length 257; Pred. No. 1.6e+03;

90.5%;

Best Local Similarity

Query Match

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lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders, thrombocytopaenia, stem cell disorders, aplastic anaemia, for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating oscepoprosis, osteoarthritis, bone degenerative disorders, or periodontal disease, lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, diabetes mellitus, myasthenia gravis), allergic reactions and conditions, such as asthma or other respiratory problems, coagulation disorders, bowel disease, viral infection and are useful in altering bodily bowel disease, viral infection and are useful in altering bodily characteristics. The present sequence represents a novel protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical faugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                               Score 19; DB 22; Length 264;
Pred. No. 1.6e+03;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 35955.
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                                                                                                                                                                                                                                                                                                                                                                               90.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           264 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 eagaas 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; dev
pharmaceutical.
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                                                                                                                                                                                                                                                                                          invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB69721;
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapphing, and in recombinant production of (II). The cand gene mapphing are also used in diagnostics as expressed sequence tags of righting expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a polosopeptide in tissue, as molecular weight markers and as a candood supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and annino acid sequences of the invention.
                                                                                                                                                                                     ö
(ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess hindivariaty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                Length 270;
                                                                                                                                               Score 19; DB 22; Length 27
Pred. No. 1.7e+03;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID No 34145; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #3777.
                                                                                                                                                                                                                                                                                                                                                   ABG03786 standard; Protein; 270 AA.
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                                                                                                                                                90.5%;
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73
                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                           270 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS67973.
                                                                                                                                                                                                                                                         169 eagsts 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2.
                                                                                                                                                                                                                         1 eagxxs 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                       ABG03786;
                                                                                             Sequence
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AAU47789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in
Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cartilage, tendon and/or nerve tissue growth or regeneration;
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                                                                                                                                                                                                                           Score 19; DB 22; Length 270;
Pred. No. 1.7e+03;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted protein #1635.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
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                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                270 AA;
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                                                                                                                                   Sequence
                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (syndrits, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. Pracence is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies polypeptides may be used as antigens in the production of antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as chagnostic agents for determining P. acnes presence, for example, by conzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed and contactive in the contactive intention of a pating o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthtalnitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                 ö
Length 273;
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                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes immunogenic protein #8685.
Score 19; DB 22; L
Pred. No. 1.7e+03;
); Mismatches 2;
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID No 8984; 1069pp; English.
                                                                                                                                                                                                                                                               AAU47789 standard; Protein; 290 AA.
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, Jen S,
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
90.58;
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> J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-616774/71.
N-PSDB; AAS59539.
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  Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                              1 eagxxs
                                                                                                                                           35 eagass
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Length 305;

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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clsories involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human consistic amino acid sequences of the invention.
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                   Length 290;
   , DB 22; Le.,
. 1.8e+03; Indels
                 Score 19; DB;
Pred. No. 1.8e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #2072.
                                                                                                                                                                                                         ABG02081 standard; Protein; 305 AA.
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                 90.5%;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                             13-FEB-2002 (first entry)
                                                    Conservative
Query Match
Best Local Similarity
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                                                                                                                    79 eagass 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001
                                                                                                                                                                                                                                           ABG02081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13638 and AAH13633 to AAH13642 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto J;
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0
                                        Indels
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, Otsuki T;
Score 19; DB 22; L
Pred. No. 1.9e+03;
); Mismatches 2;
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Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                   Human protein sequence SEQ ID NO:16523.
                                                                                                                                                                                                       AAB94964 standard; Protein; 323 AA
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90.58;
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                              (first entry)
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                                      Conservative
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   Query Match
Best Local Similarity
Matches 4; Conserv
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323 AA;

Sequence

28

Matches

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Regulating mucus secretion by a mucus-secreting cell, useful for treating e.g. bronchitis, asthma or pneumonia, by administering a compound that inhibits or enhances myristolated alanine-rich C-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of human myristoylated alanine-rich C kinase substrate MARCKS protein, a major cellular substrate. The invention relates to methods of inhibiting mucus secretion by a mucus. Secreting cell by administering a compound that inhibits MARCKS protein-related mucus secretion. Such compounds include active fragments of MARCKS protein such as MANS peptide (see AAY95897) and MA-PDS peptide (see AAY95897), which corresponds to a phosphorylation site of MARCKS. The inhibitor compounds can be used to treat conditions such as bronchitis, cystic fibrosis, chronic obstructive pulmonary disease, asthma, emphysema, pneumonia, influenza, rhinitis and the common cold. An alternative sequence for MARCKS is provided in AAY95899, which differs from the present sequence at 2 amino acid residues, Ala-84 (Ser) and
                                                                 MARCKS; myristoylated alanine-rich C kinase substrate; human; mucus secretion; inhibitor; bronchitis; asthma; cystic fibrosis; chronic obstructive pulmonary disease; pneumonia; empysema; influenza; rhinitis; therapy.
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Pred. No. 2e+03;
0; Mismatches 2; Indels
                                  Human myristoylated alanine-rich C kinase substrate MARCKS.
                                                                                                                                                                                                                          'note= "Ser in sequence of AAY95899"
                                                                                                                                                                                                                                                             /note= "Ala in sequence of AAY95899"
                                                                                                                                                                                                                                                                                                                                /note= "MA-PSD peptide of AAY95897"
                                                                                                                                                                                                                                                                               2..25
/note= "MANS peptide of
152..176
                                                                                                                                                                                            Location/Qualifiers
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20-NOV-2000 (first entry)
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Best Local Similarity 66.7
Matches 4; Conservative
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N-PSDB; AAA50339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    substrate protein
                                                                                                                                                                                          Key
Misc-difference
                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211
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                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-1999;
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                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mammalian proteins binding high density lipoprotein sub-class 3 DNA encoding them and derived antibodies, for screening potentially therapuetic HDL analogues and for diagnosing risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The protein product may be used to raise Abs, and the CDNA to create probes, both useful in screening for HDL analogues, agonists and antagonists, and in identifying abnormalities in the HDL binding/receptor pathway. HDL analogues can be used in treating hypercholestrolaemia and atherosclerosis
                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                             High density lipoprotein; HDL-binding protein; atherosclerosis; hypercholesterolaemia; ds.
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                                DB 22; Length 323;
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                                                                  Indels
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                                                                                                                                                                                                                                                                                                                            High density lipoprotein (HDL) binding protein.
                              Score 19; DB 22;
Pred. No. 2e+03;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2e+03;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19;
                                                                                                                                                                                                                       AAR05528 standard; protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY95898 standard; Protein; 332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 1A-D; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hart CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.5%;
66.7%;
                            90.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88US-0273388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV OF WASHINGTON
                                                                                                                                                                                                                                                                                           (first entry)
                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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N-PSDB; AAQ04784.
                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atherosclerosis.
                                                                                                                                     308 eagsts 313
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                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-1988;
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Gaps

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AAY95898;

29

AAY95898 RESULT

Matches

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New polynucleotides encoding human heat-shock protein-binding protein, HspBP-1 and HspBP-2, useful for investigating the effects of heat shock-protein regulation -
                                                                                                                              Zebrafish; heat shock protein binding protein; HspBPF; development; apoptosis; cellular stress; heart disease; cancer;
                                                                                                       Zebrafish Hsp-binding protein HspBPF.
                          AAY97409 standard; Protein; 333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guerriero V, Raynes DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GUER/) GUERRIERO V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-400030/34.
N-PSDB; AAA38747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RAYN/) RAYNES D A.
                                                                                                                                                                                  Brachydanio rerio.
                                                                                                                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                      Misc-difference
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                                                                             14-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                              02-JUN-2000
                                                  AAY97409;
                                                                                                                                                          hypoxia
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                AAY97409
RESULT
                                                    The present sequence is that of human myristoylated alanine-rich C kinase substrate MARCKS protein, a major cellular substrate. The invention relates to methods of inhibiting mucus secretion by a mucus secreting cell by administering a compound that inhibits MARCKS protein-related mucus secretion. Such compounds include cardive fragments of MARCKS protein such as MANS peptide (see AAY95897) and MA-PDS peptide (see AAY95897), which corresponds to phosphorylation site of MARCKS. The inhibitor compounds can be used to treat conditions such as bronchlits, cystic fibrosis, chronic obstructive pulmonary disease, asthma, emphysema, pneumonia, influenza, rhinitis and the common cold. An alternative sequence for MARCKS is provided in AAY95898, which differs from the present sequence at 2 amino acid residues, Ser-84 (Ala) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Regulating mucus secretion by a mucus-secreting cell, useful for treating e.g. bronchitis, asthma or pneumonia, by administering a compound that inhibits or enhances myristolated alanine-rich C-kinase
                                                                                        MARCKS; myristoylated alanine-rich C kinase substrate; human; mucus secretion; inhibitor; bronchitis; asthma; cystic fibrosis; chronic obstructive pulmonary disease; pneumonia; empysema; influenza; rhinitis; therapy.
                                                                 Human myristoylated alanine-rich C kinase substrate MARCKS.
                                                                                                                                                                                                                                 /note= "Pro in sequence of AAY95898"
2..25
/note= "MANS peptide of AAY95896"
152..176
                                                                                                                                                                                                         /note= "Ala in sequence of AAY95898"
                                                                                                                                                                                                                                                                                     /note= "MA-PSD peptide of AAY95897"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 46-47; 66pp; English.
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNC-) UNIV NORTH CAROLINA STATE.
                                                                                                                                                                                                                                                                                                                                                                24-FEB-2000; 2000WO-US05050.
                                                                                                                                                                                                                                                                                                                                                                                        99US-0256154,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Martin LD, Adler KB;
                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-572036/53.
N-PSDB; AAA50340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             substrate protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 AA;
                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                             WO200050062-A2
                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        24-FEB-1999;
                                      20-NOV-2000
                                                                                                                                                                                                                                                                                                                                        31-AUG-2000
              AAY95899;
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GAC"

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/label= unknown /note= "encoded /label= unknown

/note= "encoded by GAG"

98US-0109351 99WO-US27651

/label= unknown /note= "encoded by GAA"

Location/Qualifiers

(first entry)

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                                                                                                                                                                                                                                                                                       Gaps
                                    The present sequence is the sequence for the zebrafish heat shock protein-binding protein (HspBPF), which is involved in the regulation of the heat shock proteins, which are components of the development, apoptosis and cellular stress pathways. The human homologue is useful not only for research into these areas, but also for treating disorders such as heart disease, hypoxia and cancer.
                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                          90.5%; Score 19; DB 21; Length 333; 66.7%; Pred. No. 2e+03; ive 0; Mismatches 2; Indels
Disclosure; Page 35-36; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG90789 standard; Protein; 341 AA.
                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
                                                                                                                                                                                  333 AA;
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                                                                                                                                                                                  Sequence
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Gaps

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Score 19; DB 21; Length 332; Pred. No. 2e+03; ); Mismatches 2; Indels

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Conservative

206 eagaas 211

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1 eagxxs

90.5%; 66.7%;

Query Match Best Local Similarity

Matches

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Pompejus M, Kroeger B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of nucleotide and protein as sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                       Ochiai K, Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum; homeostasis; adaptation; HA protein; fine chemical production; organic acid; proteinogenic amino acid;
                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; SEQ ID NO: 4543; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum HA protein sequence SEQ ID NO:176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.5%; Score 19; DB 22; Length 341; 66.7%; Pred. No. 2.1e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                     Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                                         C glutamicum protein fragment SEQ ID NO: 4543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB79110 standard; Protein; 341 AA.
                                                                                                                                                                                                                                                                                                        (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                           99JP-0377484.
                                                                                                                                                                                                            18-DEC-2000; 2000EP-0127688.
                                                                                                                                                                                                                                                          07-APR-2000; 2000JP-0159162.
                                                                                                                     Corynebacterium glutamicum.
           (first entry)
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 AA;
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239 eagtss 244
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                                                                                                                                                  EP1108790-A2
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           26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                     Nakagawa
Tateishi
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nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; genetic engineering; Brevibacterium; environmental condition.
                                                                                                                                                                                                                                                                                                                                99DE-1032128.
99DE-1032129.
99DE-1032226.
99DE-1032920.
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99DE-1032935.
99DE-1032973.
99DE-1033002.
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99DE-1032924
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                                                                                                       Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BADI ) BASF AG.
                                                                                                                                        WO200100842-A2.
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14-JUL-1
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14-JUL-1
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Schroeder H, Zelder O, Haberhauer G;

WPI; 2001-061974/07 N-PSDB; AAF71225.

New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins

Claim 20; Page 383-384; 712pp; English.

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AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis and adaptation (HA) proteins given in AAB79023 to AAB79242. The c. glutamicum HA genes (1) can be used in vectors for expression in host cells and production of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or pyrimidine base, nucleoside, nucleotide, light, saturated or unsaturated tatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, polyketide or enzyme. The amino acids produced can be lysine, glutamine, glutamine, aparine, aspartate, glycine, serine, threonine, methionine, tyrosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (1) or HA proteins encoded by then are used for dlagnosing the presence or activity of Corynebacterium diphtheriae. (1) can be used to map the C. glutamicum genome or can be used as markers for genetically engineered Corynebacterium or previbacterium. The HA proteins encoded by the (1) are used to maintain homeostasis in C. glutamicum or help the microorganism to adapt to different environmental conditions.

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nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins
                                                          Claim 20; Page 466-467; 712pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KONN ) GIST-BROCADES BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fungus; food processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Den Hombergh JPTW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-042197/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 eagtss 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 eagxxs 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW44368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum; homeostasis; adaptation; HA protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; acarbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; genetic engineering; Brevibacterium; environmental condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids,
                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum HA protein sequence SEQ ID NO:244.
                                                            DB 22; Length 341;
                                                          Score 19; DB 22; Length 34
Pred. No. 2.1e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                           AAB79144 standard; Protein; 341 AA.
                                                          90.5%;
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99DE-1032128
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99DE-1032922
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99DE-1033002
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                                                                                                                                                                                                                                                                                                                                                                           30-APR-2001 (first entry)
                                                                                                    4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99DE-103
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                                                          Query Match
Best Local Similarity
341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF71259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200100842-A2.
                                                                                                                                                                                    239 eagtss 244
                                                                                                                                           1 eagxxs 6
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                                                                                                                                                                                                                                                                                                                                    AAB79144;
  Sequence
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and adaptation (HA) proteins given in AAB79023 to AAB79242. The call adaptation (HA) proteins given in AAB79023 to AAB79242. The cells and production of fine chemicals, such as, an organic acid, cells and production of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, polyketide or enzyme. The amino acids produced can be lysine, glutamine, glutamate, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tryosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (I) or HA proteins encoded by then are used for diagnosing the presence or activity of Corynebacterium diphtheriae. (I) can be used to map the C. glutamicum genome or can be used as markers for genetically engineered Corynebacterium or presentine. The HA proteins encoded by the (I) are used to maintain homeostasis in C. glutamicum or help the microorganism to adapt to different environmental conditions.
AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metallo-protease deficient fungus with site selected DNA disruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus nidulans; metallo-protease; pepH; protein degradation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 22; Length 34...
Pred. No. 2.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus nidulans metallo-protease pepH.
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describes a new protease deficient filamentous fungus, optionally with reduced extracellular acid protease activity, containing a site selected disruption of DNA resulting in reduced metallo-protease activity. The fungi are useful for the production of (heterologous and homologous) proteins e.g. for food processing, since reduced protease activity. The fundialses the chance that, and rate at which, the proteins are degraded withinses the chance that, and rate at which, the proteins are degraded used to production. DNA sequences encoding metallo-proteases activity as used to produce metallo-protease activity. They are also used to produce metallo-protease activity. They are also useful for producing filamentous fungia with reduced metallo-protease activity. They are also useful for producing filamentous fungia metallo-protease. By culturing filamentous fungia transformed with the constructs under suitable conditions for sequence expression and recovering the metallo-protease. Such metallo-proteases are useful to assess in vitro whether proteins which it is proposed to produce from a fungal host are susceptible to the protease, so determining which metallo-protease genes need to be
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Aspergillus nidulans from the present invention. The present invention
                                                                                                                                                                                                                                                                                                           inactivated in the host. They are also useful in industrial processes
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The pre-pro neutral protease II is derived from Aspergillus oryzae and is the precursor to neutral protease II. The neutral protease II can be expressed in Saccharomyces cerevisae and can be produced efficiently and in a secreted form.
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0
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Pred. No. 2.1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neutral protease II gene from Aspergillus - used to produce recombinant enzyme by expression in Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "mature neutral protease II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR14147 standard; Protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89JP-0336737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pre-pro neutral protease II
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                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant enzyme.
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                                                                                                                                                                                                                                                                                                                                                 349 AA;
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237 eagsts 242
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                                                                                                                                                                                                                                                                                                                                                   Sequence
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prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella premioniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen corporate for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trawick JD,
   Length 352;
                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa cellular proliferation protein #346.
                                 Indels
                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
Score 19; DB 12; L
Pred. No. 2.2e+03;
0; Mismatches 2;
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Seq ID No 11949; 511pp; English.
                                                                                                                                                                       AAU36356 standard; Protein; 363 AA.
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2000US-257931P.
2001US-269308P.
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2000US-207727P.
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                               Conservative
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                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa.
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Query Match
Best Local Similarity
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                                                                                           240 eagsts 245
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                                                               1 eagxxs 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto RT,
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                                                                                                                                             RESULT 37
                               Matches
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AAG20561 standard; Protein; 377 AA.
                                                115 eagtas 120
                 1 eagxxs 6
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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                      Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding plant lignin biosynthesis enzymes – used to transform plants to modulate lignin biosynthesis
                                                                                  ;
                                               90.5%; Score 19; DB 22; Length 363; 66.7%; Pred. No. 2.2e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 96-97; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang X;
                                                                                                                                                                                                                                   AAY05663 standard; Protein; 366 AA.
                                                                                                                                                                                                                                                                                                                                     Maize caffeic O-methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC.
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97US-0057082.
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                                                                                  4; Conservative
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N-PSDB; AAX25202.
                                               Query Match
Best Local Similarity
Matches 4; Conserv
363 AA;
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                                                                                                                 1 eagxxs 6
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27-AUG-1997;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                               Arabidopsis thaliana protein fragment SEQ ID NO: 22802.
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Score 19; DB 20; Length 366; Pred. No. 2.2e+03; 0; Mismatches 2; Indels

90.5%; ilarity 66.7%; Conservative (

Query Match Best Local Similarity Matches 4; Conserv

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Pred. No. 2.3e+03;
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Gaps

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  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 52052.
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  AAG41800
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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29-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                  24-SEP-1999;
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Matches
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PR 22-UN 1999; 99US 014035.

PR 23-UN 1999; 99US 014035.

PR 24-JUN 1999; 99US 014035.

PR 24-JUN 1999; 99US 014035.

PR 24-JUN 1999; 99US 014031.

PR 29-UN 1999; 99US 014031.

PR 29-UN 1999; 99US 014031.

PR 01-UL-1999; 99US 0141287.

PR 01-UL-1999; 99US 0141287.

PR 13-UL-1999; 99US 014234.

PR 13-UL-1999; 99US 0142320.

PR 13-UL-1999; 99US 0142320.

PR 13-UL-1999; 99US 014232.

PR 13-UL-1999; 99US 014232.

PR 13-UL-1999; 99US 014332.

PR 13-UL-1999; 99US 0144085.

PR 13-UL-1999; 99US 0144085.

PR 13-UL-1999; 99US 0144085.

PR 13-UL-1999; 99US 014408.

PR 13-UL-1999; 99US 014408.

PR 13-UL-1999; 99US 014408.

PR 13-UL-1999; 99US 014408.

PR 22-UL-1999; 99US 014408.

PR 22-UL-1999; 99US 014408.

PR 23-UL-1999; 99US 014710.

PR 23-
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Gaps
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Pred. No. 2.4e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP70581 standard; Protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protease biosynthetic protein.
9905-0151303.
99075-0151303.
99075-01513130.
99075-01513150.
99075-01513158.
99075-01513158.
99075-0155139.
99075-0155139.
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990S-0161405
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990S-0161360
990S-0161360
990S-0161992
990S-0161993
990S-0161993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 90.5%;
Local Similarity 66.7%;
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycosis; yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| |
|eagaas 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eagxxs 6
 30 - AUG - 1999;
31 - AUG - 1999;
07 - SEP - 1999;
10 - SEP - 1999;
15 - SEP - 1999;
16 - SEP - 1999;
22 - SEP - 1999;
23 - SEP - 1999;
24 - SEP - 1999;
25 - SEP - 1999;
26 - SEP - 1999;
27 - SEP - 1999;
28 - SEP - 1999;
29 - SEP - 1999;
06 - OCT - 1999;
07 - OCT - 1999;
07 - OCT - 1999;
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1-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-1991
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25-OCT-1999;
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29-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 42
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Gaps

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Human serine protease inhibitor from cDNA clone HETDK50; fusion protein; serpin; serine protease; human pre-alpha-1-antitrypsin precursor; extracellular matrix degradation; multiple sclerosis; cancer; arthritis; inflammation; immune system disorder; neurodegenerative disorder; Kallmann's syndrome; Down's syndrome; Alzheiner's; secreted protein; galactorrhea; hypogonadism; somatostatin; protein purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a serine protease inhibitor (serpin) from CDNA clone HETDK50 which is obtained from human endometrial tumour tissue cDNA library. The protein shows a high degree of sequence similarity to human pre-alpha-1-antitrypsin precursor. The serpin and its coding sequence are used in the diagnosis and treatment of disorders related to abnormal level of the protein or mutation in the nucleotide sequence. The serpin can be used for treating disorders characterised by degradation of extracellular matrix, e.g. cancer, arthritis, multiple sclerosis and immune system disorders, for treating wasting associated
immunogenic compositions as vaccines. Vectors containing C. pneumonia nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human serine protease and serpin polypeptides, used to develop products for treating e.g. immune disorders, cancers, inflammation, transplant rejection or infections, or as food
                                                                                                                                 Length 393;
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20..422
/label= Mature_serine_protease_inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                            Human serine protease inhibitor from cDNA clone HETDK50.
                                                                                                                                 Score 19; ____ Pred. No. 2.4e+03; ____ 2;
                                                                                                                               Score 19; DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Pages 83-85; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                             AAY28643 standard; Protein; 422 AA.
                                                                                                                                                               ;
                                                                                                                               90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0073961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US02292
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                  especially where the vect epitope of C. pneumoniae.
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-508502/42.
                                                                                                                                                Best Local Similarity
                                                                               393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX80907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                             101 eagsss 106
                                                                                                                                                                                                1 eagxxs 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9940183-A1
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                                                                                                                                                                                                                                                                                                                                             AAY28643;
                                                                                   Sequence
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ni J,
                                                                                                                                                                                                                                                                              44
                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                               AAY28643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                         Product is a biosynthetic component involved in the synthesis of protease. The protein may be produced from a transformed S.cerevisiae expression system for the large scale production of protease.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                              Protease prodn. - by culturing microorganism transformed with vector derived from saccharomycosis.
                                                                                                                                                                                                                                                                                                                                                           Length 390;
                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 8; Length 390
Pred. No. 2.4e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia pneumoniae transmembrane protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 1016; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY35147 standard; Protein; 393 AA.
                                                                                                                                                                                                             Disclosure; Fig 1; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                           90.5%;
                 85JP-0244893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0107078.
97FR-0014673.
                                               85JP-0244893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 66.7 les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-357842/30.
                                                                                                              WPI; 1987-173695/25.
                                                                                                                                                                                                                                                                                                             390 AA;
                                                                                                                               N-PSDB; AAN70927
                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 eagsss 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                           1 eagxxs 6
                                                                               (FUKU/) FUKUI
               31-OCT-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09927105-A2
                                             31-OCT-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY35147;
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43
                                                                                                                                                                                                                                                                                                                                                                          Best Loca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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(PPIMs) given in AAB74668 to AAB74694. The PPIMs can have activities such as: anti-human immunodeficiency virus (HIV); antidiabetic: antithyroid:
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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      δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; protease; protease inhibitor; protease and protease inhibitor; antidiabetic; immunostimulati; anti-human immunodeficiency virus; HIV; antidiabetic; immunostimulator; antidialmatory; antitityroid; immunosuppressive; immunosoulator; antidout; thyronimmetic; cytostatic; antibacterial; fungicide; protozoacide; antiarteriosclerotic; antiabeteriosclerotic; antipacnimic; virucide; hepatotropic; gene therapy; autoimmune disorder; inflammatory disorder; AIDS; DiGeorge's syndrome; severe combined immunodeficiency disease; SCID; Chediak-Higashi syndrome; Cushing's disease; Addison's disease; autoimmune thyroiditis; gout; Crohn's diseases; Hashimoto's thyroiditis; Sjodrome; infection; Grave's syndrome; cell proliferative disorder; arteriosclerosis;
with excessive protease production during inflammation or neurodegenerative disorders e.g. Kallmann's and Down's syndromes, Alzheimer's and Huntington's diseases. It may also be used to reduce excess levels of prolactin in the treatment of galactorrhea and hypogonadism, and decrease the amount of free circulating somatostatin's inhibitory effect on the release of growth hormone. The fusion of this protein to His-tag, HA-tag, 1gG domains, etc. facilitates protein purification and fusion to 1gG-1, 1gG-3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF81714 to AAF81740 encode the human proteases and protease inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New protease (inhibitors) useful for diagnosis and treatment of autoinmune/inflammatory disorders such as acquired immunodeficiency syndrome, Cushing's disease, Addison's disease and cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lu DAM;
                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                              Score 19; DB 20; Length 422;
Pred. No. 2.6e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cirrhosis; hepatitis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protease and protease inhibitor PPIM-24.
                                                                                                                                   albumin increases the half life time in vivo.
                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            AAB74691 standard; Protein; 422 AA.
                                                                                                                                                                                                              90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0147986.
99US-0160807.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry).
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-202760/20.
                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAF81737
                                                                                                                                                                                                                                                                                                            370 eagaas 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-1999;
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                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yue H,
                                                                                                                                                                                                                                                                                                                                                            45
                                                                                                                                                                                                                                                Matches
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refines of the first care and processor care and the first care and prevention of autoimmune/inflammatory disorders such as AIDS, DiGeorge's syndrome, care combined immunodeficiency disease (SCID), Chediak-Higashi syndrome, Cushing's disease, Addison's disease, autoimmune thyroiditis, Crohn's disease, Hashimot's thyroiditis, Siogren's syndrome, wiral, bacterial, impal, parasitic, processor, and helminthic infections and cell proliferative disorder such as arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis and cancer. PPIM polynucleotide sequences can be used in somatic or germline gene therapy and in diagnosis of diseases. They can also be used in generating subtribution probes useful in mapping the naturally occurring genomic sequences and in molecular biology techniques.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                Length 422;
                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 22; Length 42. Pred. No. 2.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 51488.
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG41388 standard; Protein; 427 AA.
                                                                                                                                                                                                                                                                                                                                                                              90.5%;
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990S-0123180.
99US-0123180.
99US-0125788.
99US-0126264.
99US-0127625.
99US-0127625.
99US-0128714.
99US-0130871.
99US-0130871.
99US-0130871.
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 eagaas 375
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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06-APR-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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990S-0145913.
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990S-0146388.
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99US-0142920.
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99US-0144814.
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99US-0141842.
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99US-0147493
               10 - JUN - 1999;
14 - JUN - 1999;
16 - JUN - 1999;
17 - JUN - 1999;
18 - JUN - 1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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                                                      Gaps
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                         Score 19; DB 21; Length 435;
Pred. No. 2.7e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 27565.
                                                                                                                                                                        AAG24040 standard; Protein; 440 AA.
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99US-0123180.
99US-0123548.
99US-0125788.
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990S-0134256.
990S-0134218.
990S-0134219.
990S-0134221.
                         Query Match 90.5%;
Best Local Similarity 66.7%;
Matches 4; Conservative
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99US-0127462.
99US-0128234.
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99US-0132485.
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29-OCT-1999;
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Matches 4; Conserv
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15-SEP-1999;
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30 - AuG - 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant infectious bovine rhinotracheitis virus - provides isolated DNA encoding gpE glyco:protein, gpG glyco:protein and unique short 2 genes of the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.5%; Score 19; DB 14; Length 441; 66.7%; Pred. No. 2.7e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                          IBR glycoprotein E gene; unique short 2 gene.
                                                                                                                                             Sequence encoded by glycoprotein G gene.
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AAR31955 standard; Protein; 441 AA.
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N-PSDB; AAQ36768.
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                                                                                              06-JUN-1993
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Perfect score: Sequence:

Run on:

Scoring table:

Searched:

Database

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APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
TITLE OF INVENTION: Polypeptides and Their Uses
CORRESPONDENCES: 534
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DoS
SOFTWARE: FastSEO for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
US-08-990-571-52
US-07-796-361A-11
US-08-348-891A-2
US-08-358-817-2
US-08-505-817-2
US-08-505-817-1
US-08-506-834-1
US-08-506-834-1
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Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 345, Application US/08936165A
Patent No. 6348582
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P50549
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APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTONNEY,AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lonetto, Michael
Nicholas, Richard
Pratt, Julie
Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PSC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFEAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hodgson, John
Knowles, David
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CITY: King of Prussia
STATE: PA
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TELEFAX: 61
TELEX:
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21, Appl
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 1008
Listing first 50 summaries
                                                                                        OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Patent No. 5885772
GENERAL INFORMATION:
APPLICANT: Aderem, Alan A.
APPLICANT: Chen, Jianmin
APPLICANT: Chen, Sandy
TITLE OF INVENTION: METHOD FOR THE DETECTION OF ANENCEPHALX
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                 APPLICANT: Hook, Magnus
APPLICANT: Patti, Joseph M.
APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Sthanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFIRE TO S.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURKENI AFFLICATION DATE:

APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION UNBER: 33,928
REGISTRATION UNBER: TAMK:193
TELEPHONE: (512) 418 3000
TELEPHONE: (512) 414 3000
TELEPHONE: (512) 414 3000
TELEPHONE: (512) 414 3000
TELEPHONE: (512) 414 3000
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66.7%; Pred. No.
                                                                                                                   Sequence 4, Application US/08856253; Patent No. 6288214; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: Klauber & Jackson 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 EAGTSS 39
       28 EAGTSS 33
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US-08-405-175A-5
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                                                                          RESULT 3
US-08-856-253-4
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APPLICANT: Patti, Joseph M.
APPLICANT: House-Pompeo, Karen
APPLICANT: Sthanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 4; Length 159;
Pred. No. 3.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                 90.5%; Score 19; DB 4; Length 47; 66.7%; Pred. No. 93; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: CONCURTENTLY HERWITH
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFENNCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/08856253; Patent No. 6288214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 159 amino acids
TYPE: amino acid
STRANDEDNESS:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                        STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-936-165A-345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, Wi
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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US-08-856-253-2
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APPLICANT: HOOK, I
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Texas COUNTRY: U.S. ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                        31 EAGATS 36
                                                                                                                                                                                                                                                                                                                            1 eagxxs 6
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US-08-856-253-2
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                                                                                                                                                                                             Score 19; DB 1; Length 4**.
Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 2; Length 441
Pred. No. 8.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mark D. Cochran
APPLICANT: Richard D. Macdonald
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotracheltis Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,949B
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 678
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: John P. White
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPPY disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/08185949B Patent No. 5874279 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 6, Application US/08856253
                                        21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0525
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.5%;
                TELEX: 422523
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441 amino acids
(212) 391-0525
                                                                                                                                                                                               Query Match
Best Local Similarity 66.79
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                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-191-866D-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                               265 EAGSAS 270
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US-08-185-949B-21
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APPLICANT: Macdonald, Richard D.
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotracheitis Virus S-IBR-052 And Uses Thereof
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted primary structure of human MARCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 2; Length 332;
Pred. No. 6.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING.SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,866D
FILING DATE: 4 February 1994
                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,175A
FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REFERENCE/POCKET NUMBER: 26,742
REFERENCE/POCKET NUMBER: 600-1-121A
TELECOMMUNICATION INFORMATION:
TELEFAN: 201 343-1684
TELEFAX: 201 343-1684
TELEFX: 201 343-1684
TELEX: 201 343-1684
TELEX: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/08191865D Patent No. 5783195
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 90.5
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                          COMPUTER READABLE FORM:
                    New Jersey
Hackensack
                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 |
206 EAGAAS 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; HYPOTHETICAL:
US-08-405-175A-5
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US-08-191-866D-21
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                                    COUNTRY:
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GENERAL INFORMATION:
APPLICANT Gianturco, S.H.
APPLICANT: Bradley, W.A.
TITLE OF INVENTION: B Receptor Gene and Protein
TITLE OF INVENTION: B Receptor Gene and Protein
FILE REFERENCE: D5880
CURRENT APPLICATION NUMBER: US/09/130,242B
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: MS WORD, Macintosh OS 8.5
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Fatent No. 5851794
GENERAL INFORMATION:
APPLICANT: GUSS, Bengt
APPLICANT: JONSSON, Hans
APPLICANT: JONSSON, Hans
APPLICANT: JONSSON, Hans
APPLICANT: JOSEPH
APPLICANT: SIGNAS, Christer
APPLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 5; Length 908;
Pred. No. 1.8e+03;
0; Mismatches 2; Indels
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66.7%; Pred. No. 2.1e+03;
ive 0; Mismatches 2;
                          APPLICATION NUMBER: PCT/US95/03747
FILING DATE: 27-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
REPERENCE/DOCKET NUMBER: FP-LJ 1453
REPERENCE/OCKET NUMBER: FP-LJ 1453
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Sequence 2, Application US/09130242B
: Patent No. 6194558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.5%;
   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.5
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-130-242-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear PCT-US95-03747-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 EAGSSS 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 EAGTAS 332
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US-09-130-242-2
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                       GENERAL INFORMATION:

APPLICANT: Hook, Magnus
APPLICANT: Hook, Magnus
APPLICANT: House-Pompoo, Karen
APPLICANT: Sthanam, Narayana
APPLICANT: Symersky, Jindrich
TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 4; Length 512;
Pred. No. 1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application PC/TUS9503747
GENERAL INFORMATION:
APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INFORMATION: Brevican, A Glial Cell Proteoglycan
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/856,253
FILING DATE: Concurrently Herewith
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STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDAER: US 60/017,678
FILING DATE: 16-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: TAMK:193
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas COUNTRY: U.S. 21P: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 512 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 60...
A: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-856-253-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
Patent No. 6288214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 EAGTSS 154
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PCT-US95-03747-3
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RESULT 12
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ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.5%; Score 19; DB 2; Length 1183; 66.7%; Pred. No. 2.3e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/08485355B
Patent No. 6177075
GENERAL INFORMATION:
APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik,
TITLE OF INVENTION: Insect Viruses and Their Uses in
Protecting Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                 ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/485,355B
                                                                                                                                                                                                                                                                                           FILING DATE: 22-MAY 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 21-AUG-1992
PRIOR APPLICATION NUMBER: WO PCT/SE91/00707
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9003374-7
FILING DATE: 22-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE-DOCKET NUMBER: 012899-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,031A
FILING DATE: 22-MAY-1995
                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONVEXT: United States
2IP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1183 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 57
                                                                            STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                            COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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US-08-485-355B-31
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            APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELECX: 910 277299
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
FURNALL OF TREESTICES:
FUNDAMENTERISTICS:
F
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Patent No. 5869270
GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.
APPLICANT: Wide, Jin-An
APPLICANT: Wong, Hing
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,387B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 4;
Pred. No. 1.7e+05;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-08-485-3558-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: PATIONSON DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/283,302
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66./°,
Loc 4; Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Deerfield
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 eagxxs 6
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                                                                    Score 18; DB 4; Length 59; Pred. No. 2.2e+02; J. Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.7%; Score 18; DB 5; Length 59; 66.7%; Pred. No. 2.2e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NOATH: PCT/US95/09816A
FILING DATE: 31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: STR-4665-CIP2 TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
TELEPAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,302
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: PEATSON, LOUISE S.
REGISTRATION NUMBER: 32,369,666-07
                                                                                                                                                                                                                                                                                        Sequence 109, Application PC/TUS9509816A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dade International, Inc. STREET: 1717 Deerfield Road
                                                                                                                                                                                                                                                                                                                             APPLICANT: Wong, Hing C.
APPLICANT: Rhode, Perter R.
APPLICANT: Widanz, Jon A.
APPLICANT: Grammer, Susan
APPLICANT: Grammer, Ana C.
APPLICANT: Chavaillaz, Pierre-Andre
APPLICANT: Jiao, Jin-An
                                                                                                             .;
0
                                                                      85.7%;
66.7%;
                                                 Ouery Match
Best Local Similarity 6b.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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PCT-US95-09816A-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1717 Deer
CITY: Deerfield
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: un}
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                     RESULT 14
PCT-US95-09816A-109
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              US-09-067-615-109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rhode, Peter R.
APPLICANT: Rhode, Jin-An
APPLICANT: Jiao, Jin-An
APPLICANT: Burkhardt, Martin
APPLICANT: Wong, Hing
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dade International, Inc.
STREET: 1717 Deerfield Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60015
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/596,387
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
PRIOR APPLICATION NUMBER: US 08/283,302
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: PEATSON, LOUISE S.
REGISTRATION NUMBER: 32,369
REGISTRATION NUMBER: 32,369
REGISTRATION NUMBER: STR-4665-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
TELEPHONE: (708) 267-5300
TELEPHONE: (708) 267-5376
INFORMATION FOR SEG ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                   STR-4665-CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/067,615
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 109, Application US/09067615 Patent No. 6309645 GENERAL INFORMATION:
NAME: Pearson, Louise S.
REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: STR-4/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
TELEPAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 anino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY:
                                                                                                                                                                                                                                                                                                           85.7%;
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66...
Loc 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS: unknown unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Deerfield
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino ac
STRANDEDNESS:
TOPOLOGY: unkr
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41 EAGRAS 46
                                                                                                                                                                                                                                                                                                                                                                                         1 eagxxs 6
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US-09-067-615-109
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Length 66;
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Pred. No. 2.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Croce, Carlo M.
APPLICANT: Hobner, Kay
TITLE OF INVENTION: FHIT PROTEINS AND NUCLEIC ACIDS AND
TITLE OF INVENTION: METHODS BASED THEREON
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MCMASIERS, DANBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 100084.406
FELECOMMUNICATION INFORMATION:
TELECHNONE: (206) 622-4900
FELECAMUNICATION INFORMATION:
TELECHNONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
"WIND: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUNTRY: New York
COUNTRY: U.S.A.
2 IP: 10036-2711
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/598,873
FILING DATE: 09-FEB-1996
CLASSTETCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FRIEDEL, THORMATION:
NAME: FRIEDEL, THORMATION:
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8666-004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08598873; Patent No. 5928884; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9000
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7°,
'-haq 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear US-08-446-137B-10
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                                       Sequence 12, Application US/08446137B
Fatent No. 6162903
GENERAL INFORMATION:
APPLICANT: Trowern, Androws.
APPLICANT: Murphy, Jonathan P.
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: And SERD Laurence, Oliver S.
ADDRESSEE: SEED and BERRY LLP
STREEF: 6500 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-446-137B-10

Sequence 10, Application US/08446137B

Sequence 10, Application US/08446137B

Sequence 10, Application US/08446137B

GENERAL INFORMATION:
APPLICANT: Trowern, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Laurence, Oliver S.
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Pred. No. 2.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMINICATION INFORMATION:
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 60...
4; Conservative
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STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; STRANDEDNESS:
; TOPOLOGY: 11
US-08-446-137B-12
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                       US-08-446-137B-12
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Gaps

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TITLE OF INVENTION: Expressing Proteins that Recognize and Adhere to Specific TITLE OF INVENTION: Probes
NUMBER OF SEQUENCES: 5
NUMBER OF SEQUENCES: ADDRESS: ADDRESSEE: Kenneth A. Weber
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUMTRY: USA
ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08446137B

Patent No. 6162903

GENERAL INFORMATION:
APPLICANT: Trowern, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Laurence, Oliver S.
APPLICANT: SEQUENCES: L.
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.7%; Score 18; DB 1; Length 123; 66.7%; Pred. No. 4.6e+02; 1ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/446,137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15280-10
                                                                                                                                                                                           2IP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 32,334
REFERENCE/POCKET NUMBER: 1528
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 123 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-07-869-912-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 EAGGSS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 eagxxs 6
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                                                                                       Length 91;
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                                                                                    Score 18; DB 2; Length 91;
Pred. No. 3.4e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Croce, Carlo M.
APPLICANT: Huebner, Kay
TITLE OF INVENTION: FHIT PROTEINS AND NUCLEIC ACIDS AND
TITLE OF INVENTION: METHODS BASED THEREON
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/605,430
FILING DATE: 22-FEB-1996
CLASSIFICATION: 536
ATTORNEY/GENT INCORATION:
NAME: Friebel, Thomas E.
REGISTRATION NUMBER: 29,258
REGISTRATION NUMBER: 8666-005
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEX: 66141 PENNIE
TELEX: CAL44 PENNIE
TELEX: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/08605430 Patent No. 6242212 GENERAL INFORMATION:
                                                                                  85.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 91 amino acids
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-605-430-19
; MOLECULE TYPE: peptide US-08-598-873-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                              49 EAGKSS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 EAGKSS 54
                                                                                                                                                                         1 eagxxs 6
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                                                                                                                                                                                                                                                                                                   US-08-605-430-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-869-912-2
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RESULT 22
US-09-423-340-2
US-09-423-340-2
Sequence 2, Application US/09423340
Patent No. 6225454
GENERAL INDOFMATION:
APPLICANT: MIXAGI, Taeko
APPLICANT: WADA, Tadashi
APPLICANT: WOSHIKAWA, YUKO
TITLE OF INVENTION: SIALIDASE LOCALIZED IN PLASMA MEMBRANE AND
TITLE OF INVENTION: SIALIDASE LOCALIZED IN PLASMA MEMBRANE SIALIDASE LOCALIZED IN PLASMA MEMBRANE
FILE REFERENCE: OP699
CURRENT APPLICATION NUMBER: US/09/423,340
CURRENT FILING DATE: 1999-11-22
EARLIER FILING DATE: 1999-11-22
SEALIER FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 24
SEQ ID NOS: 24
SEQ ID NOS: 24
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US-08-749-902-1
; Sequence 1, Application US/08749902
; Patent No. 5985635
; GENERAL INFORMATION:
APPLICAMY: Bandman, Olga
; APPLICAMY: Goli, Surya K.
; APPLICAMY: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
; TITLE OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 4; Ler
Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0150 US
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: The Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.7'
Best Local Similarity 66.7'
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT; ORGANISM: Bos primigenius US-09-423-340-2
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                                          25 EAGSGS 30
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  1 eagxxs 6
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85.7%; Score 18; DB 2; Length 211;
Best Local Similarity 66.7%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                          Length 175;
                                                                                                                                                                                                                                                                                                                                        Score 18; DB 4; Length 175
Pred. No. 6.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
US-08-708-958-2
Sequence 2, Application US/08708958
Fatent No. 5948952
GENERAL INFORMATION:
APPLICANT: SANDS, Arthur T.
APPLICANT: BRADLEY, Allan
APPLICANT: BRADLEY, Allan
APPLICANT: BRADLEY, Allan
APPLICANT: ABUIN, Alejandro
TITLE OF INVENTION: XERODERMA PICMENTOSUM-DEFICIENT
TITLE OF INVENTION: MOUSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,958
FILING DATE: SEP-1996
CLASSIFICATION: 424
ATTORNEY/ACENT INFORMATION:
NAME: KIT, GORDON
NAME: KIT, GORDON
NAME: KIT, GORDON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 PENNSYLVANIA AVENUE, N.W. CITY: WASHINGTON STAFF. D.C. COUNTRY:
           NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6641
TELEPHONE: (202) 293-7060
TELEPHONE: (202) 293-7060
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-708-958-2
                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-446-137B-9
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20037
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GENERAL INFORMATION:

APPLICANT: Petre, Dominique
APPLICANT: Cerbelaud, Edith
APPLICANT: Mayaux, Jean-Francois
APPLICANT: Applicant: Mayaux, Jean-Francois
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: NOVEL POLYPEPTIDES, THE DNA SEQUENCES
TITLE OF INVENTION: ALLOWING THEIR EXPRESSION, METHOD OF PREPARATION, AND
TITLE OF INVENTION: UTILIZATION
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.7%; Score 18; DB 4; Length 500;
66.7%; Pred. No. 1.8e+03;
ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATORIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/612,673
FILING DATE: 19901114
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 29-OCT-1997
CLASSIFICATION: 536
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                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTIESS, PETER F
REGISTRATION NUMBER: 33,860
REFRENCE/CDCKET NUMBER: 4800
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fotter, Jane E.R. REGISTRATION NUMBER: 33,332 REFERENCE/DOCKET NUMBER: 03 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I Street, N.W. CITY: Washington, D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
      Diskette
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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Best Local Similarity
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      MEDIUM TYPE:
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US-07-612-673-2
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APPLICANT: Kikkoman Corporation
APPLICANT: Kikkoman Corporation
TITLE OF INVENTION: Leucine Aminopeptidase Gene, Recombinant DNA, and
TITLE OF INVENTION: Process for Producing Leucine Aminopeptidase
FILE REFERENCE: PH-622
CURRENT APPLICATION NUMBER: US/09/330,095
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: JP-164611/1998
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ DI NOS: 14
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                                                                                                                                                                                                                                                      Score 18; DB 2; Length 433
Pred. No. 1.6e+03;
0; Mismatches 2; Indels
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Pred. No. 1.8e+03;
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.
APPLICANT: Accreded, Jorge
APPLICANT: Burkhardt, Martin
APPLICANT: Jiao, Jin-an
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-960-190A-25; Sequence 25, Application US/08960190A; Patent No. 6232445
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 24
US-09-330-095-1
'S Sequence 1, Application US/09330095
'Patent No. 6127161
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                      85.78;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.7%;
66.7%;
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US-09-330-095-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.7
Best Local Similarity 66.7
Matches 4; Conservative
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COMPUTER READABLE FORM:
                                                                                                                          TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: Consensus
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
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US-08-749-902-1
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LENGTH: 481
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Gaps

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Sequence 52, Application US/08990571

Batent No. 6214971

GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 4; Length 503
Pred. No. 1.8e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Burns, Doane, Swecker and Mathis STREET: The George Mason Building, Washington & STREET: Prince Streets
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILLING DATE: US/08/990,571

FILLING DATE: 11-DEC-1997
                                                                                                                                                                                                                                                    ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/07796361A Patent No. 528829.
GENERAL INFORMATION:
GENERAL THFORMATION:
APPLICANT: YEH, Patrice
APPLICANT: MAYANX, Jean-Francois APPLICANT: CERBELAUD, Edith
APPLICANT: PETRE, Dominique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORIGINAL SAURS: Babesia Microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503 amino acids
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                        USA
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      417 EAGGTS 422
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US-07-796-361A-11
                                                                RESULT 28
US-08-990-571-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G. APPLICANT: Lodes, Michael J. APPLICANT: Lodes, Michael J. APPLICANT: Houghton, Raymond APPLICANT: Sleath, Paul R. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.7%; Score 18; DB 4; Length 503; 66.7%; Pred. No. 1.8e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                 Length 503;
                                                                                                                                                                                                                               Score 18; DB 1; Length 503
Pred. No. 1.8e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24 APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.426C1
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52, Application US/08845258 Patent No. 6183976 GENERAL INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                               85.78;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Babesia Microti
US-08-845-258-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 503 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             Query Match 85.7
Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                  , MOLECULE TYPE: protein US-07-612-673-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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STREET: 63
                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-845-258-52
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APPLICANT: SASAKI, Keiko
APPLICANT: MORI, Takayuki
APPLICANT: MAKINO, Satoshi
TITLE OF INVENTION: ATTENDATED MEASLES VIRUS VACCINE,
TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 521;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,891A
FILING DATE: 25-NOV-1994
CLASSIFICATION NUMBER: US 07/848,400
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-293625
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATCH: Andrew J.
REFERENCE/DOCKET NUMBER: 32 925
REFERENCE/DOCKET NUMBER: XP-7501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%; Score 18; DB 1; I
66.7%; Pred. No. 1.9e+03;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                              03715.0010-01000
APPLICATION NUMBER: US 07/612,673 FILING DATE: 14-NOV-1990
                                                                                            APPLICATION NUMBER: FR 8916332
FILING DATE: 11-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
FEFERENCE/DOCKET NUMBER: 03715.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08348891A Patent No. 5654136
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STREET: 745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 521 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-539-666-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO:
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                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 EAGGSS 172
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APPLICANT: Cerbelaud, Edith
APPLICANT: Cerbelaud, Edith
APPLICANT: May way, Jean-Francois
APPLICANT: Hay, Patrice
TITLE OF INVENTION: No. 5766918e1 Polypeptides, The DNA Sequences
TITLE OF INVENTION: Allowing their Expression, Method of Preparation, and
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
CORRESPONDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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Pred. No. 1.9e+03;
0; Mismatches 2; Indels
                                                                COMPUTER READABLE FURG:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/796,361A
FILING DATE: 19911122
CLASSIFICATION 19735
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90-14 853
FILING DATE: 28-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CRANE-FEURY, SHARON E.
REGISTRATION NUMBER: P36,113
PRECISTRATION NUMBER: P36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Washington
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
- APPLICATION NUMBER: US 08/097,009
FILING DATE: 27-JUL-1993
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08539666
Patent No. 5766918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 521 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
       United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 440580,
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 85.7
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-796-361A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 30
US-08-539-666-2
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APPLICANT: Saito, Yoshinasa
APPLICANT: Saito, Yoshinasa
APPLICANT: Ishii, Yoshinori
APPLICANT: Ishii, Xoshinori
APPLICANT: Ishii, Xoshinori
APPLICANT: Suzuki, Hiromi
TITLE OF INVENTION: 0. 5753481e1 L-sorbose Dehydrogenase and No. 5753481e1
TITLE OF INVENTION: Dehydrogenase Obtained from Gluconobacter oxydans T-100
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 Jefferson Davis Highway, Suite 400
STATE: Virginia
COUNTRY: USA
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        Gaps
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        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: EDBAP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,841
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
PRICK APPLICATION NUMBER: US/08/513,841
FILING DATE: 01-NOV-1995
FILING DATE: 08-MAR-1993
PRICK APPLICATION NUMBER: US/08/51/1993
FILING DATE: 28-SEP-1993
ATTORNEY APPLICATION NUMBER: JP 241851/1993
REGISTRATION NUMBER: JS-24,618
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-909-0 PCT
TELECOMMUNICATION NUMBER: 18-909-0 PCT
TELECOMMUNICATION NUMBER: JS-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 1; Ler
Pred. No. 1.9e+03;
      5;
        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: mat peptide
; COCATION: 1..530
US-08-513-641-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Gluconobacter oxydans
STRAIN: T-100
                                                                                                                                                                              Sequence 1, Application US/08513841 Patent No. 5753481 GENERAL INFORMATION:
      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%;
                                                                                                                                                                                                                                         Niwa, Mineo
Saito, Yoshimasa
Ishii, Yoshinori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85.7
Best Local Similarity 66.7
Matches 4; Conservative
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                 263 EAGLAS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 EAGVTS 369
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                                            1 eagxxs 6
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      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SASAKI, Keiko
APPLICANT: MORI, Takayuki
APPLICANT: MORI, Takayuki
APPLICANT: MARINO, Satoshi
TITLE OF INVENTION: ATTENUATED MEASLES VIRUS VACCINE,
TITLE OF INVENTION: TIS ABSOLUTE IDENTIFICATION
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
                                                                                                                                                                                                ö
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 2; Length 525; Pred. No. 1.9e+03;
                                                                                                                                                            Length 525;
                                                                                                                                        Score 18; DB 1; Length 222
Pred. No. 1.98+03;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,817
FILING DATE: 04-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,891
FILING DATE: 25-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,400
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 3-293625
FILING DATE: 14-CCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, ANGTEW J.
REGISTRATION NUMBER: 32,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: KP-7501A
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08905817
Patent No. 5824777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: YOUNG & THOMPSON 745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%;
66.7%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 525 amino acids
amino acid
                    : 525 amino acids
amino acid
SEQUENCE CHARACTERISTICS
LENGTH: 525 amino acid
                                                                             ; MOLECULE TYPE: protein US-08-348-891A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arlington
                                                                                                                                                                                                                                                                       263 EAGLAS 268
                                                                                                                                                                                                                                       1 eagxxs 6
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                                                                                                                                                                                                                                                                                                                                  RESULT 32
US-08-905-817-2
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APPLICANT: Saito, Yoshinasa
APPLICANT: Ishii, Yoshinori
APPLICANT: Ishii, Yoshinori
APPLICANT: Yoshida, Masaru
APPLICANT: Suzuki, Hiromi
TITLE OF INVENTION: No. 5861292e1 L-sorbose Dehydrogenase and No. 5861292e1
TITLE OF INVENTION: L-sorbosone Dehydrogenase Obtained from Gluconobacter
TITLE OF INVENTION: oxydans T-100
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C. STREET: 1755 Jefferson Davis Highway, Suite 400
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                                                                                                                                                                                                                                                                                                                               ZIP: 22202
COMPUTER READABLE FORM:
MEDLIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS additor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.7%; Score 18; DB 2; 1 ilarity 66.7%; Pred. No. 1.9e+03; Conservative 0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFFLICATION NUMBER: US/US/942,0/3

CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 08/513,841
FILING DAYE: 01-NOV-1995
APPLICATION NUMBER: UK 9304700.9
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9304700.9
FILING DATE: 08-SEP-1993
ATORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 18-909-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: 703-413-220
TELEFRAN: 703-413-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ); NAME/KEY: mat peptide
); LOCATION: 1..530
US-08-942-673-1
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US-09-118-317-1
Sequence 1, Application US/09118317
Patent No. 6197562
GENERAL INFORMATION:
APPLICANT: NIWA, Mineo
APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshimasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Gluconobacter oxydans STRAIN: T-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1:00 acids TOPOLOGY: 1:00 acids TOPOLOGY: 1:00 acid
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                     STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                 APPLICANT: Niva. Mineo
APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshimasa
APPLICANT: Ishii, Yoshimasa
APPLICANT: Yoshida, Masaru
APPLICANT: Yoshida, Masaru
APPLICANT: Yoshida, Masaru
APPLICANT: Hayashi, Hiromi
TITLE OF INVENTION: Method for Producing 2-Keto-L-Gulonic Acid
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: Olon, Spivak, McClelland, Maier & Neustadt,
ADDRESSEE: P.C.
STREET: Alinghway, Suite 400
CITY: Alinghia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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66.7%; Pred. No. 1.9e+03;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1..530
; IDENTIFICATION METHOD: experimentally
US-08-696-834-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,834
FILING DATE: 24-SEP-1996
CLASSIFFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: JP 28612/1994
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        олодицум: Gluconobacter oxydans
STRAIN: T-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3200
TELEFAX: (703) 413-220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/08942673; Patent No. 5861292; GENERAL INFORMATION: APPLICANT: Niwa, Mineo
                                                                                                 Sequence 1, Application US/08696834 Patent No. 5834263 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 66.7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 EAGVTS 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 35
US-08-942-673-1
                                                                               US-08-696-834-1
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DNA Molecules Encoding Plant
Protoporphyrinogen Oxidase and Inhibitor-Resistant Mutants
Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Johnson, Marie
APPLICANT: Volrath, Sandra
APPLICANT: Ward, Eric
APPLICANT: Ward, Eric
TITLE OF INVENTION: Protoporphyrinogen Oxidase Genes
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PapPLICATION NUMBER: US/08/808,931 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 2; Ler
Pred. No. 2.1e+03;
0; Mismatches 2;
                                                                                                                              ADDRESSEE: No. 5939602artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6018105artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-UNN-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGC 1847
                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/08808323 Patent No. 6018105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,21
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 85.7%;
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 560 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: not relevant;
MOLECULE TYPE: protein
US-08-808-931-18
                  TITLE OF INVENTION: DNA TITLE OF INVENTION: Proi TITLE OF INVENTION: Then NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10591-9005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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US-08-808-323-18
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                                     APPLICANT: Suzuki, Hiromi
TITLE OF INVENTION: No. 6197562el L-sorbose Dehydrogenase and No. 6197562e
TITLE OF INVENTION: No. 6197562el L-sorbose Dehydrogenase and No. 6197562e
TITLE OF INVENTION: Oxydans T-100
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: USA
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Pred. No. 1.9e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS-DOS Editor CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/118,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513,841
FILING DATE: 01-NOV-1995
APPLICATION NUMBER: 0K 9304700.9
FILING DATE: 08-MAR-1993
APPLICATION NUMBER: UK 9304700.9
FILING DATE: 08-MAR-1993
APPLICATION NUMBER: JP 241851/1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 24,618
RESIGNED/COCKET NUMBER: 18-909-0 PCT
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3000
TELEPAX: 248855 OPAT 0:
INFORMATION FOR SEQ 1D NO: 1:
SENGRALIA
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Patent No. 5939602
GENERAL INFORMATION:
APPLICANT: Volrath, Sandra
APPLICANT: Johnson, Marie
APPLICANT: Potter, Sharon
APPLICANT: Ward, Eric
APPLICANT: Heifetz, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Gluconobacter oxydans STRAIN: T-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 85.7%;
Best Local Similarity 66.7%;
Matches 4; Conservative
                  Yoshida, Masaru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 530 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IDENTIFICATION METHOD:
US-09-118-317-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat peptide LOCATION: 1..530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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364 EAGVTS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 eagxxs 6
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Gaps
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APPLICANT: Voltrath, Sandra
APPLICANT: Johnson, Marie
APPLICANT: Ward, Eric
APPLICANT: Halferz, Peter
TITLE OF INVENTION: HERBICIDE-TOLERANT PROTOPORPHYRINGEN
TITLE OF INVENTION: OXIDASE ("PROTOX")
CORRESPONDENCES: 43
CORRESPONDENCES: 43
CORRESPONDENCES: No. 6084155artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%; Score 18; DB 3; Length 560 ilarity 66.7%; Pred. No. 2.1e+03; Conservative 0; Mismatches 2; Indels
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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,420B
FILING DATE: 22-JUN-1998
CLASSIFICATION: 800
                 PRIOR TOWN NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
FILING DATE: 28-FEB-1996
FILING DATE: 28-FEB-1996
FILING DATE: 21-UN-1996
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 09/059,164
FILING DATE: 13-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/050,603
FILING DATE: 30-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 40
2.09-102-420B-18
3. Sequence 18, Application US/09102420B
5. Patent No. 6084155
                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
REFRENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8689
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
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Best Local Similarity
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COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,603A
FILING DATE: 30-MAR-1998
CLASSILCATION: 800
                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Volrath, Sandra
APPLICANT: Volrath, Marie
APPLICANT: Johnson, Marie
APPLICANT: Potter, Sharon
APPLICANT: Ward, Eric
APPLICANT: Heifetz, Peter
TITLE OF INVENTION: DNA Molecules Encoding Plant
TITLE OF INVENTION: Protoporphyrinogen Oxidase
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 6023012artis Corporation
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APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-UN-1996
ATTORNEY AGENT INFORMATION:
NAME: Meigs, J Timothy
REGISTATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: GGC 1846
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAR: (919) 541-8689
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-050-603A-18; Sequence 18, Application US/09050603A; Patent No. 6023012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                       CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                             FILING DATE:
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APPLICATION NUMBER: 09/102,420
FILING DATE: CUDROWN>
APPLICATION NUMBER: US 09/050,603
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: US 60/126,430
FILING DATE: 11-MAR-1998
APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-JUN-1996
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Medis, J. Timothy
REGISTRATION NUMBER: 38,21
REFERENCE/DOCKET NUMBER: GG 1847/CIP3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/419,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 4;
Pred. No. 2.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SELHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3330 HILLVIEW AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: NO. 6308458 Relevi;
STRANDEDNESS: NO. 6308458 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-497-698-18
                          28-FEB-1996
28-FEB-1996
21-JUN-1996
06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08419078
Patent No. 5587306
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
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Patent No. 6308458
GENERAL INFORMATION:
APPLICANT: Volrath, Sandra
Johnson, Marie
Ward, Eric
Heifelz, Peter
TITLE OF INVENTION: HERBICIDE-TOLERANT PROTOPORPHYRINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%; Score 18; DB 3; Length 560;
66.7%; Pred. No. 2.1e+03;
Live 0; Mismatches 2; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: No. 6308458artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                  PRIOR AFFLICATION NAMER: US 08/808,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION NUMBER: US 60/012,705
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,003
FILING DATE: 20-FUN-1996
PRIOR APPLICATION NUMBER: US 60/020,003
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: GC 1847/CIP3
FELEFAN (919) 541-8689
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,698
FILING DATE: 03-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OXIDASE ("PROTOX")
APPLICATION NUMBER: US 60/126,430 FILING DATE: 11-MAR-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: CURNOWN>
30-MAR-1998
11-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 560 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US. ZIP: 27709
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APPLICANT: Sumant CHENGAPPA
APPLICANT: Sumant CHENGAPPA
APPLICANT: Sumant CHENGAPPA
APPLICANT: John S. REID
APPLICANT: Jacqueline DE SILVA
TITLE OF INVENTION: No. 5981831el Exo-(1-4)-Beta-D Galactanase
NUMBER OF EXQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: O.S.A.
COMPUTER: BM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,944
FILING DATE: 23-AUG-1996
CLASSIFICATION DATA:
CONTON BATH.
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                                                                                                    Length 566;
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Pred. No. 2.7e+03;
0; Mismatches 2; Indels
                                                                                                  Score 18; DB 1; Length 566 Pred. No. 2.1e+03; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00372
FILING DATE: 23 FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9403423.8
FILING DATE: 23-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: HOSKins, Joann
APPLICANT: Jaskunas, S. Richard
APPLICANT: Rockey, Pamela K.
APPLICANT: Zhao, Genshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 45
US-08-731-716-2
'Sequence 2, Application US/08731716
'Patent No. 5789202
                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08696944 Patent No. 5981831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 730 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: TYPE: protein
US-08-696-944-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                Query Match 85.7
Best Local Similarity 66.7
Matches 4; Conservative
: No. 5676946e
9118
                                                                                                                                                                                                           111 |
338 EAGAQS 343
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    LIBRARY:
                       ; CLONE: S
US-08-726-883-2
                                                                                                                                                                                                                                                                                      RESULT 44
US-08-696-944-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,883
FILING APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/419,078
FILING DATE: 10-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08726883
; Sequence 2, Application US/08726883
; Patent No. 556546
; GEMERAL INFORMATION:
APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFEREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE INCYTE PHARMACEUTICALS, INC.
STRET: 3330 HILLVIEW AVENUE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: LUTHER, BARBARA J.
REGIETRATION UNDBER: 33954
REFERENCE/DOCKET NUMBER: PF0030 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                 PF0030 US
              ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTATION NUMBER: 3954
REFERENCE/DOCKET NUMBER: PFOO
TELECOMMUNICATION INFORMATION:
TELEFRAX: 415-855-0572
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 annino acids
TYPE: amino acid
STANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 566 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                       ; LIBRARY: NO. 5587306e
; CLONE: 9118
US-08-419-078-2
                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein IMMEDIATE SOURCE:
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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338 EAGAQS 343
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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GENERAL INFORMATION:
APPLICANT: Pot, David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Jefferson, Anne Bennett
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6001354el Grb2 Associating Protein and Nucleic
TITLE OF INVENTION: Acids Encoding Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                  APPLICANT: Dalton, Stephen
APPLICANT: Rochan, Jarema P
APPLICANT: Rochan, Mark A
TITLE OF INVENTION: METHOD TO DETECT PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 1;
Pred. No. 3.5e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-1995
                                                                                                                                              Sequence 14, Application US/08434730 Patent No. 5637463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08560005 Patent No. 6001354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Semionow, Raina
REGISTRATION NUMBER: 39022
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (201)235-4391
TELEPAX: (201)235-2363
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 968 amino acida
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-434-730-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Dalton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 0. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                               Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      711 EAGVTS 716
                                           321 EAGSGS 326
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    1 eagxxs 6
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                                                                                                       RESULT 47
US-08-434-730-14
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US-08-560-005-2
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TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLECTIDE
TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
CURRENT APPLICATION NUMBER: US/09/651,656
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 60/192,764
NUMBER OF SEQ ID NOS: 106
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Pred. No. 3e+03;
0; Mismatches 2; Indels
        APPLICANT: No. 57892021s, Franklin H.
TITLE OF INVENTION: Penicillin Binding Protein From
TITLE OF INVENTION: Streptococcus Pneumoniae
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-651-656-19
Sequence 19, Application US/09651656
Patent No. 6340566
GENERAL INFORMATION:
APPLICANT: MCCUTHEN-MALONEY, SANDRA
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 1; I
Pred. No. 2.7e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: x-10,887
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/731,716
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
Rosteck, Paul R. Jr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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66.7%;
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 731 amino acids
amino acid
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Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                            STREET: Lilly Corport CITY: Indianapolis STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-651-656-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                           COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 EAGALS 107
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SEQ ID NO 19
LENGTH: 823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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Gaps

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SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,540
FILING DATE: 14-OCT-1999
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TELECOMMNICATION: INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/560,005
FILING DATE: 17-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dow, Karen B. REGISTRATION NUMBER: 29,684
                  INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 976 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         976 amino acids
                                                                                                                                                                                                                  Query Match 85.7
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-418-540-2
                                                                                                                                      MOLECULE TYPE: protein US-09-195-868-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                  496 EAGVTS 501
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STATE: Ca
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: KAVANAUGH MD, MICHAEL
APPLICANT: POT PH.D., DAVID
APPLICANT: WILLIAMS MDPHD, LEWIS T.
TITLE OF INVENTION: SIGNALING INOSITOL POLYPHOSPHATE
TITLE OF INVENTION: 5-PHOSPHATASES (SIPS)
                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-0624000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPRAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
APPLICATION NUMBER: US/09/195,868
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocial
                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09195868 Patent No. 6090621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4560 HORTON STREET
CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 11.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-923-2707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.78;
66.78;
                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: FIRESTONE, LEIGH H. REGISTRATION NUMBER: 36,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               : 976 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-560-005-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
San Francisco
California
                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
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                                        USA
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STATE: CA
COUNTRY: USA
THE 94608
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                                                          94105
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US-09-195-868-14
                                        COUNTRY:
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ö Sequence 2, Application US/09418540
Patent No. 6296848
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pot, David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Milliams, Lewis T.
APPLICANT: Milliams, Philip W.
TITLE OF INVENTION: No. 6296848el Grb2 Associating Protein and Nucleic UNMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000 Gaps ó ö Length 976; 85.7%; Score 18; DB 4; Length 976; 66.7%; Pred. No. 3.6e+03; ive 0; Mismatches 2; Indels 85.7%; Score 18; DB 3; Length 976 66.7%; Pred. No. 3.6e+03; .ive 0; Mismatches 2; Indels

Search completed: August 30, 2002, 15:04:45 Job time: 8556 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model	August 30, 2002, 15:00:04; Search time 26.93 Seconds (without alignments) 21.409 Million cell updates/sec	SK-853-CLAIM4 sagxxs 6	BLOSUM62 Gapop 10.0 , Gapext 0.5	283138 segs, 96089334 residues	Total number of hits satisfying chosen parameters: 283138	Lh: 0 Lh: 2000000000
GenCore Copyright (c) 1993	otein search, using s	August 30, 2002, 19	BASK-853-CLAIM4 21 1 eagxxs 6	BLOSUM62 Gapop 10.0 , Gapext	283138 seqs, 960893	hits satisfying chos	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
	OM protein - pro	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of	Minimum DB seq length: 0 Maximum DB seq length: 2(

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 50 summaries

Database :

## SUMMARIES

	Description	adhesin - Staphylo	hypothetical prote		٦	_	ч			Œ	two-component resp	two-component resp		hypothetical prote	probable exported		hypothetical prote	3	coat protein - soy	coat protein - soy	hypothetical prote	ATP phosphoribosyl	transcription acti	hypothetical prote	₽	myristylated alani	neutral proteinase	probable adenylate		O	•
SUMMARIES	ID	A48620	AF2563	C84320	B72627	F82189	T11215	T29807	T23855	A70844	AD1560	AF1202	AH0459	E84169	AE1029	T48058	B90026	G87721	JC1071	S18931	H82638	D64070	A56235	S38091	149529	A38873	S16547	G95872	T01571	A83177	
	DB	7	7	7	~	~	~	7	7	7	~	~	7	7	~	~	~	7	7	7	7	Н	7	~	~	~	7	ď	7	7	
	Length	37	83	122	143	145	164	200	201	204	212	212	220	245	246	257	260	263	266	267	302	303	311	322	323	332	352	352	357	363	
dР	Query																												90.5		
	Score	19	19	19	19	19	19	19	19	19	19			19		19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	
	Result No.	-	7	Э	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	

amino acid transpo hypothetical prote 3-isopropylmalate	hypothetical prote cAMP response elem acid proteinase (E dihydrolipoamide s	dihydrolipoamide s glycine betaine AB glycine betaine AB	probable processin CAMP receptor CAR4 glycoprotein gX - hynotherical prote	hypotherical prote major facilitator hypothetical prote	nodulation protein nodulation protein probable transcrip probable membrane
T47240 E83800 I40226	T25452 A39429 UT0334 E72068	C86556 AD1559 AF1201	B72778 A54813 S35783	D85438 C87629 D70853	S08384 S10133 T41039 S54536
363 2 365 2 367 1	387 2 389 1 390 2	393 2 397 2	403 2 4443 2 458 2	462 2 469 2 474 2	4 8 8 2 2 4 8 8 2 2 8 4 9 9 2 2 8 9 2 2 8 9 9 9 9 9 9 9 9 9 9 9
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30 31 32	ლ ო ო ლ ო ო ტ ტ ტ	37 38 39	444 01196	4444 4450	444 449 50

## ALIGNMENTS

RESULT 1 A46620 adhesin - Staphylococcus aureus (fragment) C;Species: Staphylococcus aureus (fragment) C;Species: Staphylococcus aureus C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995 C;Accession: A6620 R;Patti, J.M.; Boles, J.O.; Hook, M. Biochemistry 32, 11478-11435, 1993 A;Title: Identification and biochemical characterization of the ligand binding domain A;Reference number: A48620; MUID:94032261 A;Accession: A48620 A;Accession: A4
Query Match Best Local Similarity 66.7%; Pred. No. 89; Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Oy 1 eagxxs 6
Db 16 EAGTSS 21 RESULT 2 AF2563 APpothetical protein as18505 [imported] - Anabaena sp. (strain PCC 7120) plasmid pCC7
C. Species: Anabaena sp. A. Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C. Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C. Accession: AP2563 R. Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Suginoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001 A, Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840 A; Accession: AF2563
A;Status; prelininary A;Nolecule type: DNA A;Residues: 1-83 <kur> A;Residues: 1-83 <kur> A;Cross-references: GB:AP003604; PIDN:BAB77424.1; PID:g17134868; GSPDB:GN00183 A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: as18505</kur></kur>

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A;Residues: 1-145 <HEI>A;Cross-references: GB:AE004231; GB:AE003852; NID:99656027; PIDN:AAF94690.1; GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype Bl Tor
C;Genetics:
A;Gene: VC1536
A;Map position: 1
                                                             "" protective protective vision (limported) - vidio cholerae (strain Nibybi serogroup Ol) ("Species: Vibrio cholerae ("Species: Vibrio cholerae ("Species: Vibrio cholerae ("Species: New Yord 2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 ("Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 ("Species: 18-Aug-2000 "Species: New Yord 20-Ye is Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. R. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 Arritle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUID:20406833 A; Status: preliminary A; Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 5 - Streptomyces glaucescens
C;Species: Streptomyces glaucescens
C;Species: Streptomyces glaucescens
C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: T11219
R;Summers, R.G.; Ali, A.; Shen, B.; Wessel, W.A.; Hutchinson, C.R.
B;Summers, R.G.; Ali, A.; Shen, B.; Wessel, W.A.; Hutchinson, C.R.
A;Title: Malonyl - Ccenzyme A:acyl carrier protein acyltransferase of Streptomyces glau A;Reference number: 217254; MUID:95352622
A;Accession: T11215
A;Accession: T11215
A;Actus; preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-164 <SUM>
                                                     hypothetical protein VC1536 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C;Accession: T29807
R;Latreille, P.; Stellyes, L.
submitted to the EMBL Data Library, June 1896
A;Peference number: 220689
A;Accession: T9807
A;Reference number: 220689
A;Accession: T29807
A;Reference type: DNA
A;Residues: 1-200 <-Lar>
A;Residues: 1-200 <-Lar>
A;Residues: 1-200 <-Lar>
A;Cross-references: EMBL:U61958; PIDN:AAB03180.1; GSPDB:GN00022; CESP:C25A8.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.5%; Score 19; DB 2; I
66.7%; Pred. No. 3.7e+02;
ive 0; Mismatches 2;
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                     Dypothetical protein Vng1678h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84320
F;NGY, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T.
Jung, K.H.; Alam, M.; Freitas, T.
Arathors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Reference number: A84160; MUID:20504483
A; Reference number: A84160; MUID:20504483
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein APE1474 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: O-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: B72627
R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jan-no, K.; Takahawa, B.; Ritle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID:99310339
A; Reference number: A72450; MUID:99310339
A; Status: preliminary
A; Residues: 1-143 < KAM>
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A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1474
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C;Genetics:
A;Gene: VNG1678H
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0; Mismatches 2; Indels
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                                                                              Length 83;
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Pred. No. 3.2e+02;
0; Mismatches 2; Indels
                                                                                Db 2,
1.9e+02;
2;
                                                                                Score 19; DB 2
Pred. No. 1.9e+
0; Mismatches
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Matches 4; Conserv
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Best Local Similarity
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A; Genome: plasmid
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Fri Aug

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C; Species: Listeria innocua
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Dates: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Dates: 27-Nov-2001
C; Date: 27-Nov-2001
C; Duchaud, E.; Durand, A.; Baquero, F.; Berche, P.; Bloec
C; Dominguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
D; Jones, L.M; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.;
C; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Residues: 1-212 <GLA>
A; Residues: 1-212 <GLA>
A; Residues: 1-212 <GLA>
A; Residues: 1-212 <GLA>
A; Respenimental source: strain Clipl1262
C; Genetics:
A; Gene: Linl021
C; Superfamily: regulatory protein comA; response regulator homology
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; ok, C.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Recession: AF1202
A; Ratus: preliminary
A; Molecule type: DNA
A; Residues: 1-212 < GLA>
A; Rosidues: 1-212 < GLA>
A; Residues: GB:NC_003210; PIDN:CAC99100.1; PID:g16410424; GSPDB:GN00177
A; Experimental source: strain EGD-e
C; Genetics:
C; Genetics:
C; Superfamily: regulatory protein comA; response regulator homology
                                                                                                                                                                                                     two-component response regulator, in particular B. subtilis YvqC protein homolog linl
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AF1202
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Pred. No. 4.7e+02;
0; Mismatches 2;
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Pred. No. 4.7e+02;
0; Mismatches 2;
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Conservative
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                                                            153 EAGTAS 158
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gettles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Naturer, S.; Stelton, S.; Squares, S. Aruthors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
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A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: moaE3
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A;Reference number: 219808
A;Reference number: 219808
A;Accession: T23855
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-201 <WIL>
A;Coss.references: EMBL:278015; PIDN:CAB01436.1; GSPDB:GN00023; CESP:R02D5.7
A;Experimental source: clone R02D5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein R02D5.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Spate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23855
R;Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable moaE3 protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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Pred. No. 4.5e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                   Length 200;
                                                                                                                                                                   Score 19; DB 2; Leng
Pred. No. 4.4e+02;
A;Experimental source: strain Bristol N2; clone C25A8 C;Genetics: A;Gene: CESP:C25A8.2 A;Map position: 4 A;Map position: 4 A;Introns: 173/3
                                                                                                                                                                                                                                                      0; Mismatches
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illarity 66.7%;
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Matches 4; Conserv
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Matches 4; Conserv
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A; Map position: 5
A; Introns: 174/3
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RING-HZ zinc finger protein ATL5 - Arabidopsis thaliana
N;Alternate names: protein F26K9.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Dec-2000
C;Accession: T48058
R;Bloceker, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salano submitted to the Protein Sequence Database, March 2000
A;Reference number: 224465
A;Accession: T48058
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <BLO>
A;Residues: 1-257 <BLO>
A;Cession: Telliminary
A;Residues: 1-257 <BLO>
C;Genetics:
......: Complete genome sequence of a multiple drug resistant Salmonella enterica s
A;Reference number: AB0502; PMID:11677608
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AL513382; PIDN:CAD09334.1; PID:g16505334; GSPDB:GN00176
C;Genetics:
A;Gene: STY4558
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C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: B90026
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R;Kuroda, M.; Ohta, T.; Odsyashi, N.; Sawano, T.; Tnoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; WUID:21311952; PMID:11418146
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: GB:BA000018; PID:g13702079; PIDN:BAB43371.1; GSPDB:GN00149
A; Cross-references: strain N315
C; Genetics: A; Genetics: Ge
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A,Note: F26K9.120
C;Superfamily: Arabidopsis hypothetical protein F1913.22; RING finger homology
F;109-160/Domain: RING finger homology <RRN>
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Pred. No. 5.4e+02;
0; Mismatches 2; Indels
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llarity 66.7%; Pred. No. 5.6e+02;
Conservative 0; Mismatches 2.
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Best Local Similarity
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C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: E84169
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. N.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483
A;Reference number: A84160; MUID:20504483
A;Status: preliminary
A;Residues: 1-245 <STO
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G.Species: Salmonella enterica subsp. enterica serovar Typhi
A.Note: this species has also been called Salmonella typhi
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C.Accession: AE1029
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
                                                                                                                                               ပ္ပ
                                                                                                                                                                      C; Species: Yersinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C; Accession: AH0459
R; Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A; Accession: AH0459
                                                                                                                                                   protein translocase protein TatB [imported] - Yersinia pestis (strain
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C;Genetics:
A;Gene: tatB
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Pred. No. 5.4e+02;
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; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary A; Molecule type: DNA
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A; Accession: no constant and c
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C;Species: Xylella fastidiosa
C;Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: H82638
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID: 20365717
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Mar-2000
C;Accession: D64070
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
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                                                   Submitted to the EMBL Data Library, January 1992
A; Description: CDNA sequence of the gene encoding coat protein of SMV.
A; Reference number: S18931
A; Refatus: preliminary
A; Molecule type: DNA
A; Residues: 1-267 < CGU>
A; Cross-references: EMBL:X63771; NID:g61983; PIDN:CAA45307.1; PID:g61984
C; Superfamily: tobacco etch virus genome polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 267
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Pred. No. 5.8e+02;
0; Mismatches 2; Indels
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Pred. No. 6.6e+02;
0; Mismatches 2;
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Best Local Similarity 66.7%
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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C; Accession: S18931
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                                                                                                                                                                                                                                                                                                                                                                                                           protein ZC123.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: $67721
R;Anonymous, The C. elegans Sequencing Consortium.
C;Accession: $67721
R;Anonymous, The C. elegans Sequence of the nematode C. elegans: a platform for investigating biolog A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Note: preliminary
A;Nolecule type: DNA
A;Residues: 1-263 <570.
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C;Date: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 17-Nov-2000
C;Accession: JG1071
R;Chu, R.V.; Leng, X.H.; Bao, Y.M.; Pan, N.S.; Pu, Z.Q.
Acta Bot. Sin. 34, 523-528, 1992
A;Title: Amplification of soybean mosaic virus coat protein gene by polymerase chain rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:chr_1; PIDN:AAB97603.1; PID:g2804499; GSPDB:GN00019; CESP:ZC123. A;Note: contains similarity to C2H2-type zinc fingers
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
                                                                                                                               Gaps
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Pred. No. 5.8e+02;
0; Mismatches 2; Indels
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Pred. No. 5.8e+02;
0; Mismatches 2; Indels
                                                             Length 260;
                                                          Score 19; DB 2; Length 260
Pred. No. 5.7e+02;
0; Mismatches 2; Indels
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A; Molecule type: DNA
A; Residues: 1-266 < CHU>
C; Superfamily: tobacco etch virus genome polyprotein
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Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                           Conservative
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                                                          Query Match
Best Local Similarity
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25 EAGTSS 30
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A;Gene: ZC123.3
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Best Local S:
Matches 4;
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S18931
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R: Kataoka, K.; Fujiwara, K.T.; Noda, M.; Nishizawa, M.
R: Kataoka, K.; Fujiwara, K.T.; Noda, M.; Nishizawa, M.
Rol. Cell. Biol. 14, 7581-7591, 1994
A; Title: Mafb, a new Maf family transcription activator that can associate with Maf and A; Reference number: A56235; MUID: 95021288
A; Accession: A56235
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-311 < KAT>
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Cibate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Oct-1999
Cibate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Oct-1999
Cibate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 29-Oct-1999
Cibate: 03-May-1994 #sequence_revision 03-May-1994
Cibaterion of the Protein Sequence Database, March 1994
A: Reference number: S37811
A: Reference number: S37811
A: Residues: 1-322 < DUB>
A: Residues: 1-322 < DUB>
A: Residues: 1-322 < DUB>
A: Residues: strain S288C
C: Genetics:
A: Genetics:
A: Genetics:
A: Genetics:
A: A: Residues: 11R
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 466-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630
                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Rosidues: 1-303 <TLGR>
A;Cross-references: GB:U32729; GB:L42023; NID:g1573439; PIDN:AAC22127.1; PID:g1573446;
A;Cross-references: GB:u32729; GB:L42023; NID:g1573446;
A;Note: named as homolog to a protein from Escherichia coli
C;Superfamily: ATP phosphoribosyltransferase; ATP phosphoribosyltransferase homology
C;Reywords: glycosyltransferase; histidine biosynthesis; pentosyltransferase
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C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 20-Jun-2000
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C; Genetics: #status absent
C; Superfamily: maf transforming protein; maf homology
C; Keywords: DNA binding; homodimer; leucine zipper
F; 200-289/Domain: maf homology < MAF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 1; Length 303
Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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Matches 4; Conservative
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Best Local Similarity
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Mytletrate alanine-rich protein kinase C substrate - human
Nylternate names: acidic calmodulin-binding 80k protein; MARCKS
C;Species: Homo sapiens (man)
R;Shimizu, N.
Submitted to DDBJ; September 1991
A;Reference number: A38873
A;Molecule type: mRNA
A;Reference number: A38873
A;Molecule type: mRNA
A;Residues: 1.332
A;Molecule type: mRNA
A;Reference number: A42977; MUID:93052291
A;Title: Molecular cloning and chromosomal mapping of a cDNA encoding human 80K-L pro
A;Reference number: A42977; MUID:93052291
A;Residues: 113, 47, 1732
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 113, 47, 1732
A;Status: nucleic acid sequence not shown
A;Nolecule type: mRNA
A;Residues: 113, 47, 1732
A;Residues: 113, 47, 1732
A;Status: nucleic acid sequence extracted from NCBI backbone (NCBIP:118653)
A;Residues: 113, 47, 1732
A;Note: sequence extracted from NCBI backbone (NCBIP:118653)
A;Ratlan, D.M.; Graff, J.M.; Stumpo, D.J.; Eddy Jr., R.L.; Shows, T.B.; Boyle, J.M.;
J; Biol: Chem. 266, 44399-14405, 1991
A;Reference number: A40758; MUID:91317795
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A;Residues: 1-83,'A', 85-118,'P',120-233,'W',235-286,'LVC',290,'RRGGSPRGGARGRRSLNQ',30
A;Cross-references: GB:M68956
                                                                                                                                                                                                                                                                                                                                                                                                             CSPECIES: Mus musculus (house mouse)
CSPECIES: Mus musculus (house mouse)
CSPECIES: Mus musculus (house mouse)
CSPECIES: Mar-1996 #sequence_revision 09-Mar-1996 #text_change 16-Jul-1999
CSPECIES: No. 1955
CELL 79, 1025-1034, 1994
A.Title: The mouse segmentation gene kr encodes a novel basic domain-leucine zipper the A.Title: The mouse segmentation gene kr encodes a novel basic domain-leucine zipper the A.Title: The muscression: 149529
A.Title: The muscression: 149529
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-323 ARES>
A.Cross-references: GB:L36435; NID:g625043; PIDN:AAA65689.1; PID:g625044
C.Superfamily: maf transforming proctein; maf homology
C.Steywords: leucine zipper; transcription factor
F;212-301/Domain: maf homology <AAF>
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Length 322,
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66.7%; Pred. No. 7e+02;
iive 0; Mismatches
Score 19; DB 2;
Pred. No. 7e+02;
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Best Local Similarity 66./۰
محمد 4; Conservative
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Query Match
Best Local Similarity
Matches 4; Conserv
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A; Residues: 1-352 <KUR>
A; Residues: 1-352 <KUR>
A; Residues: 1-352 <KUR>
A; Residues: 1-352 <KUR>
A; Cross-references: GB: AL591985; PIDN: CAC48647.1; PID: g15140119; GSPDB: GN00167
A; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R. L.; Hyman, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A; Reference number: A96039; MUID: 21368234; PMID: 11474104
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable N-acetylglucosamine-6-phosphate deacetylase PA3758 [imported] - Pseudomonas C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A8317
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; addman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
A; Reference number: A95842; MUID:21396508; PMID:11481431
A; Accession: 695872
A; Status: preliminary
A; Molecula +...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 7.6e+02;
0; Mismatches 2; Indels
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A;Actus: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-357 < CDEM>
A;Cross-references: EMBL:AF013294; NID:g2252848; PID:g2252871
A;Experimental source: cultivar Columbia
C;Genetics:
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Pred. No. 7.7e+02;
0; Mismatches 2;
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A;Introns: 47/3; 201/2; 243/1; 259/2
A;Note: A_TM018A10.10
C;Superfamily: Arabidosis thaliana P
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A;Genome: plasmid
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A;Molecule type: mRNA
A;Cross-references: GB:S53810; NID:9234832; PIDN:AAB19701.1; PID:9234833
R;Tatsumi, H.; Ikegaya, K.; Murakami, S.; Kawabe, H.; Nakano, E.; Motai, H.
B;Tatsumi, H.; Ikegaya, R.; Murakami, S.; Kawabe, H.; Nakano, E.; Motai, H.
A;Title: Elucidation of the thermal stability of the neutral proteinase II from Aspergil A;Reference number: S47562
A;Accession: S47562
A;Accession: S47562
A;Accession: S47562
A;Accession: S47562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 6q22.2-6q22.2
C; Superfamily: neurofilament triplet H protein
C; Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
F; 2/Modified site: myristylated amino end (9ly) (in mature form) #status predicted
F; 159, 163, 167, 170/Binding site: phosphate (Ser) (coyalent) (by protein kinase C) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable adenylate cyclase protein [imported] - Sinorhizobium meliloti (strain 1021) mag C; Species: Sinorhizobium meliloti (c; Species: Sinorhizobium meliloti (c; Species: Sinorhizobium meliloti (c; Species: Sinorhizobium meliloti (c; Species: Sinorhizobium deliloti (c; Species: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neutral proteinase II - Aspergillus oryzae
C;Species: Aspergilus oryzae
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S16547; S47562
R;Tatsumi, H.; Murakami, S.; Tsuji, R.F.; Ishida, Y.; Murakami, K.; Masaki, A.; Kawabe, Mol. Gen. Genet. 228, 97-103, 1991
A;Title: Cloning and expression in yeast of a cDNA clone encoding Aspergillus oryzae neu
                                                                                                                                                                                                                        protei
                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA
A,Residues: 189-223,'R',225-234,'E',236-322 <HER>
C;Comment: This protein is a major cellular substrate for protein kinase C and plays a
C;Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium
                                                                                 A;Note: the authors translated the codon GGC for residue 53 as Arg R;Herget, T.; Brooks, S.F.; Broad, S.; Rozengurt, E. Bur. J. Blochem. 209, 7-14, 1992
A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa or equivalent genes in different species.
A;Reference number: S29267; MUID:93011168
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66.7%; Pred. No. 7.2e+02;
ive 0; Mismatches 2; Indels
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Pred. No. 7.6e+02;
0; Mismatches 2;
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A; Residues: 176-352 <TA2>
C; Superfamily: Penicillium citrinum penicillolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GDB:118835; OMIM:177061
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ilarity 66.7%;
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Best Local Similarity
Matches 4; Conserv
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Best Local S
Matches 4
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Gaps

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C; Species: Bacillus megaterium
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: 140226; $38506
R; Meinhardt, F.; Wittchen, K.D.; Buakamp, M.
Appl. Microbiol. Biotechnol. 41, 344-351, 1994
A; Title: Cloning and sequencing of the lenc and npM genes and a putative spoIV gene f
A; Reference number: 140226; MUID: 94288995
A; Accession: 140226
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U80953; PIDN:AAB52555.1; GSPDB:GN00021; CESP:B0412.1 A;Experimental source: strain Bristol N2; clone B0412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: T25452
Cisccession: T25452
Submitted to the EMBL Data Library, December 1996
A; Beference number: Z20037
A; Reference number: Z20037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-367 <RES>
A;Cross-references: EMBL:X65184; NID:g414096; PIDN:CAA46295.1; PID:g414097
C;Genetics:
                                                                                                                                                                                                                                 RESULT 32
140226
3-isopropylmalate dehydrogenase (EC 1.1.1.85) - Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1; Length 367;
Pred. No. 7.9e+02;
0; Mismatches 2; Indels
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          Length 365;
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Pred. No. 8.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Pathway: leucine biosynthesis
C; Superfamily: 3-isopropylmalate dehydrogenase
C; Keywords: leucine biosynthesis; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein BO412.1 - Caenorhabditis elegans
       Score 19; DB 2; ]
Pred. No. 7.9e+02;
0; Mismatches 2
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A;Molecule type: DNA
A;Residues: 1-387 <BEN>
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A;Gene: CESP:B0412.1
A;Map postition: 3
A;Introns: 110/3; 146/2; 175/1; 213/2; 253/3; 318/1
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66.78;
       90.5%;
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ilarity 66.7%;
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Best Local Similarity
Matches 4; Conserv
          Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                           111 | 247 EAGTAS 252
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EAGSSS 53
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C;Function:
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathch A;Reference number: A82950; MUID:20437337
A;Accession: A83177
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-363 <STO>
A;Residues: 1-363 <STO>
A;Cross-references: GB:AE004794; GB:AE004091; NID:g9949917; PIDN:AAG07145.1; GSPDB:GN001
C;Genetics:
A;Gene: PA3758
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: 1-36 S4TO-
A; Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB04924.1; GSPDB:GN0G
A; Experimental source: strain C-125
C; Genetics:
A; Gene: BH1205
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R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Accession: E83800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid transport protein arg-1, mitochondrial [imported] - Neurospora crassa C; Species: Neurospora crassa crassa c. 5 pecies: Neurospora crassa c. 5 pecies: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000 R; Liu, O.; Dunlap, J.C. R; Liu, O.; Dunlap, J.C. A; Lif3-1174, 1996 A; Lie: Isolation and analysis of the arg-13 gene of Neurospora crassa. A; Reference number: 224416; MUID:96400914
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C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein BH1205 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-363 <LIU>
A;Cross-references: EMBL:L36378; NID:g773383; PIDN:AAC37500.1; PID:g773384
A;Experimental source: strain bdA; isolate 30-1
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Pred. No. 7.8e+02;
); Mismatches 2; Indels
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Pred. No. 7.88+02;
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A; Introns: 50/3
C; Keywords: amino acid transport; mitochondrion
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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66.7%;
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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RESULT 31

Matches

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Gaps

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Gaps

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Authors: Listeria innocua
C; Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Scocession: AD1559
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
C; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D; Jones, L.M.; Karst, U.
Science 294, 849-882, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ox, C.; Schlueter, T.; Simoces, N.; Tierrez, A.; Vacquez-Boland, J.A.; Voss, H.; Wehla
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-397 <GLA>
A; Residues: 1-397 <GLA>
A; Residues: 1-397 <GLA>
A; Residues: 1-397 <GLA>
A; Resperimental source: strain Clipli262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dividiolipoamide succinyltransferase [imported] - Chlamydophila pneumoniae (strain J1 C; Species: Chlamydophila pneumoniae, Chlamydophila pneumoniae, Chlamydophila pneumoniae, Chlamydophila pneumoniae, C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C; Accession: C86556 R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000 A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A; Reference number: A86491; MUID: 20330349
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C;Superfamily: glycine betaine/proline transport protein proV; ATP-binding cassette h
                        A)Cross-references: GB:AE001637; GB:AE001363; NID:94376807; PIDN:AAD18667.1; PID:9437 A)Experimental source: strain CWL029 C;Genetics: C,Genetics: Subs. 2 C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
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C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-393 <STO>
A; Craces: references: GB:BA000008; NID:g8978898; PIDN:BAA98733.1; GSPDB:GN00142
A; Experimental source: strain J138
C; Genetics:
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Pred. No. 8.4e+02;
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Pred. No. 8.4e+02;
0; Mismatches 2;
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Best Local Similarity
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Matches 4; Conserv
   A; Residues: 1-393 <ARN>
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                                           CAMP response element-binding protein ATF2 - rat
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Accession: A39429
R.Kageyama, R.; Sasai, Y.; Nakanishi, S.
J. Biol. Chem. 266, 15252-1531, 1991
A.Title: Molecular characterization of transcription factors that bind to the cAMP respc
A.Accession: A39429
A.Accession: A39429
A.Accession: A39429
A.Accession: A39429
A.Accession: A39429
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C.Accession: A39429
C.Accession: A39429
C.Accession: A39429
C.Scherular characterization of transcription factors that bind to the cAMP respc
A.Accession: A39429
C.Superfamily: CAMP response element-binding protein 1; fos/jun DNA-binding domain homol
C.Superfamily: CAMP response element-binding regulation
C.Superfamily: CAMP response element-binding mucleus; transcription regulation
F.231-271/Domain: fos/jun DNA-binding domain homology <FUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Saccharomycopsis fibuligera
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Sep-1999
C; Accession: J70334
R; Hindra, D; Fukui, S; Yamashita, I.
Agric: Biol. Chem. 52, 2647-2649, 1988
A; Fitle: Nucleotide sequence of the secretable acid protease gene PEPI in the yeast sacch A; Reference number: J70334
A; Accession: J70334
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Pred. No. 8.3e+02;
0; Mismatches 2; Indels
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C;Superfamily: pepsin
C;Superfamily: pepsin
C;Reywords: aspartic proteinase; hydrolase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-390/Product: acid proteinase #status predicted <MAT>
F;93,282/Active site: Asp #status predicted
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Pred. No. 8.4e+02;
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Best Local Similarity
Matches 4; Conserv
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A, Residues: 1-390 <HIR>
C, Genetics:
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354 EAGATS 359
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Advances Dictyostellum discoideum)
C; Species: Dictyostellum discoideum)
C; Species: Dictyostellum discoideum
C; Accession: A54813
R; Louis, J.M.; Ginsburg, G.T.; Kimmel, A.R.
Genes Dev. 8, 2086-2096, 1994
A; Title: The cAMP receptor CARA regulates axial patterning and cellular differentiati
A; Title: The cAMP receptor CARA regulates axial patterning and cellular differentiati
A; Title: The cAMP receptor CARA regulates axial patterning and cellular differentiati
A; Accession: A54813
A; Molecule type: DNA
A; Residues: 1-443 <LOU>
C; Generics:
A; Gene: CARA
C; Keywords: CAMP binding
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C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C;Caccession: H81455; TO2804
R;Myler, P.J; Audleman, L.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C
Proc. Natl. Acad Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein
A;Reference number: A81455; MUID:99178987
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A;Motecule type: DNA
A;Motecule type: DNA
A;Residues: 1.458 <-PYL>
A;Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24627.1; PID:g2995580; GSPDB:G
A;Experimental source: strain MHOM/IL/81/Friedlin
A;Genetics: A;Genetic
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Gispecies: bovine herpesvirus 1
Cispecies: bovine herpesvirus 1
Cispecies: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 08-Oct-1999
Gistocession: S35783
Ryadonnet, J.
Submitted to the EMBL Data Library, June 1993
Aireference number: S35782
Airecession: S35783
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Pred. No. 9.4e+02;
0; Mismatches 2; Indels
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Pred. No. 9.5e+02;
0; Mismatches 2; Indels
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C;Superfamily: pseudorabies virus glycoprotein gX
C;Keywords: glycoprotein
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Best Local Similarity
Matches 4; Conserv
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A; Molecule type: DNA
A; Residues: 1-444 <AUD>
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AF1201
C;Accession: AF1
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DNA Res. 6, 83-101, 1999
A.Fitle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A.Reference number: A72450; MUID:99310339
A.Accession: B72778
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C;Superfamily: glycine betaine/proline transport protein proV; ATP-binding cassette homd
                                                                                                                                                                                                                                                                                                                                                                                                                                          glycine betaine ABC transporter (ATP-binding protein) homolog gbuA [imported] - Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:NC_003210; PIDN:CAC99092.1; PID:g16410416; GSPDB:GN00177 A;Experimental source: strain EGD-e
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A;Molecule type: DNA
A;Residues: 1.403 «KAW>
A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79124.1; PID:g5103603
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: B72778
                                                 Gaps
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Pred. No. 8.5e+02;
0; Mismatches 2; Indels
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Pred. No. 8.6e+02;
-----has 2; Indels
                                             Indels
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C;Superfamily: mitochondrial processing peptidase alpha chain
Pred. No. 8.5e+02;
0; Mismatches 2;
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ilarity 66.7%;
Conservative
66.78;
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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Ricole, Str.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Bature 393, 537-544, 1998
Atture 393, 537-544, 1998
Atthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
Attile: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID:98295987
A; Accession: D70853
A; Accession: D70853
A; Residues: 1-474 <COL>
C; Genetics: C; GB:AL021309; GB:AL123456; NID:g3261510; PIDN:CAA16146.1; PID:e124
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R:Economou, A.; Hamilton, W.D.O.; Johnston, A.W.B.; Downie, J.A.
EMBO J. 9, 349-354, 1990
A;Title: The Rhizobium nodulation gene nodO encodes a Ca2+-binding protein that is ex A;Reference number: S08384; MUID:90151607
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C; Date: 13-4m-1995 #sequence_revision 13-Jan-1995 #text_change 29-Sep-1999
C; Accession: S10133
R; Surin, B.P.; Watson, J.M.; Hamilton, W.D.O.; Economou, A.; Downie, J.A.
Mol. Microbiol. 4, 245-252, 1990
A; Title: Molecular characterization of the nodulation gene, nodT, from two biovars of A; Reference number: S08616; MUID:90251164
A; Recession: S10133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nodulation protein nodT - Rhizobium leguminosarum plasmid pIJ1089
C;Species: Rhizobium leguminosarum
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 18-Sep-1998
                                                     hypothetical protein Rv3088 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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Pred. No. 1e+03;
0; Mismatches
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C;Superfamily: nodulation protein nodT
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Best Local Similarity 66.7%;
Matches 4; Conservative
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                                                                                                                                       C; Accession: D70853
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                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein AT4937110 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: D85438
C;Accession: B85438
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488
A;Accession: D85438
A;Accession: D85438
A;Molecule type: DNA
A;Cross-references: GB:NC_001268; NID:97270660; PIDN:CAB80377.1; GSPDB:GN00140
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                                                                                                              Length 458
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Pred. No. 9.8e+02;
0; Mismatches 2; Indels
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A;Map position: 1
C;Superfamily: Leishmania major hypothetical protein L2602.2
                                                                                                     Score 19; DB 2; Le
Pred. No. 9.7e+02;
0; Mismatches 2;
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A;Gene: CC3069
C;Superfamily: lincomycin-resistance protein lmrB
                                                                                                        90.5%;
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66.7%;
                                                                                                        Query Match 90.5
Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A; Molecule type: DNA
A; Residues: 1-469 <STO>
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                                                                                                                                                                                                                 1 eagxxs 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: AT4g37110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 eagxxs
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Gaps

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Indels

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66.7%; Pred. No. 1e+03; ive 0; Mismatches
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Job time: 585 sec
                                                     Conservative
    Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                 325 EAGATS 330
                                                                                                                                     1 eagxxs 6
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                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable transcription initiation factor Iif, alpha subunit - fission yeast (Schizosacch
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable membrane protein YDR240c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein YD8419.07c
S.Speciaes: Saccharomyces cerevisiae
C.Speciaes: Saccharomyces cerevisiae
A.Reference number: Saccharomyces
A.Reference number: Saccharomyces
A.Reference number: Saccharomyces
A.Residues: 1-492 < OLI>
A.Residues: 1-492 < OLI>
A.Residues: 1-492 < OLI>
A.Residues: BMBL:249701; NID:9817819; PID:9817826; GSPDB:GN00004; MIPS:YDR240c
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyaccession: T41039
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, December 1998
A; Reference number: 221966
A; Racession: T41039
A; Residues: 1-490 <LXN>
A; Residues: Ribb: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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A;Molecule type: DNA
A;Residues: 1-482 <SUR>
A;Residues: 1-482 <SUR>
Cross-references: EMBL:X17285; NID:g46251; PIDN:CAA35177.1; PID:g581512
C;Genetics:
A;Genetics:
A;Gene: nod7
A;Start codon: TTG
C;Superfamily: nodulation protein nod7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Superfamily: Saccharomyces cerevisiae probable membrane protein YDR240c
C;Keywords: transmembrane protein
F;119-135/Domain: transmembrane #status predicted <TWM>
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Pred. No. 1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Length 482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 2;
Pred. No. 1e+03;
0; Mismatches
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A,Introns: 180/3; 212/3
C,Reywords: transcription initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h
Similarity 66.7%;
4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.5%;
Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
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Best Local Similarity
Matches 4; Conserv
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234 EAGSAS 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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T41039
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δ 셤 bask-853-claim4.rpr

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 30, 2002, 15:06:44; Search time 13.51 Seconds (without alignments) 17.196 Million cell updates/sec Run on:

BASK-853-CLAIM4 21 1 eagxxs 6

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt\_40:\* Database :

SUMMARIES

		Descriptio	
SOLUTION		ID	
		DB	-
		Score Match Length DB	
ď	Query	Match	
		Score	
	Result	No.	

		dF			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length	BB	ΠD	Description
7	19		303	-	HIS1_HAEIN	ha
~	19		322		YK02_YEAST	
m	19		323		MAF1_MOUSE	_
4	19		323		MAF1_RAT	P54842 rattus norv
5	19		331		MACS_HUMAN	P29966 homo sapien
9	19		352		NPII_ASPOR	
7	19		363		AR13_NEUCR	
æ	19		367		LEU3_BACME	
6	19		390		CARP_SACFI	
10	19		443		CAR4_DICDI	-
11	σ		444		VGLX_HSVBS	
12	19		474		YU88_MYCTU	
13	19		482		NODT_RHILV	
14	19		487		ATF2_RAT	
15	19		561		MERA_ACICA	
16	19		561		MERA_ENTAG	P94702 enterobacte
11	19		578		AC22_STRCO	
18	19		989		DNK2_SYNY3	
19	19		638		TOXA_PSEAE	
20	19		643		SGT1_ARATH	
21	19		692		EOMD_XENLA	
22	19		883		PGCB_MOUSE	-
23	19		883		PGCB_RAT	P55068 rattus norv
24	19		806		SRCA_RABIT	_
25	19		1012		POLS_IBDVA	
56	19		1021		TSCC_HUMAN	P55017 homo sapien
27	19		1027		ISWI_DROME	Q24368 drosophila
28	19		1058		PMA1_DICDI	P54679 dictyosteli
58	19		1069		ACAA_ARATH	
30	19		1183		CNA_STAAU	
31	19	90.5	1237	Н	B3A2_MOUSE	
32	19		1262		MYO6_HUMAN	9 nm 54
33	19		1265	-	DYNA_DROME	P13496 drosophila

31 mus musculu 28 homo sapien	_	23 escherichta	80 homo sapien	32 drosophila	33 yersinia en	71 pinus pinas	94 capsella bu		_	83 bos taurus	99 mycobacteri	x5 rhizobium m	33 escherichia	66 pseudomonas	69 caenorhabdí
Q64331 092628	P53564	P22523	P39880	009332	P48633	P816	P00294	. 0149	P351	Q28183	0071	0929	P582	051466	P34469
MYO6_MOUSE	CUT1_MOUSE	MUKB_ECOLI	CUT1_HUMAN	UGGG_DROME	HMP2_YEREN	CLPA_PINPS	PLAS_CAPBU	WN14_HUMAN	PPIB_BACSU	R157_BOVIN	DUT_MYCTU	MOAE_RHIME	CEST_ECO57	FLIN_PSEAE	YMH2_CAEEL
Ц.	-	~	~		Н	Н	Н	Н	Н	٦	Н	Н	-	Н	-
1265	1395	1486	1505	1548	2035	30	66	123	143	147	154	155	156	157	159
90.5	90.5	90.5	90.5	90.5	90.5	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7
19	19	19	19	19	19	18	18	18	18	18	18	18	18	18	18
35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	20

## ALIGNMENTS

HESULT 1  HESTLET 1  HESTLET 1  AC P4385  DOT 01-NO  DO
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Cordes S.P., Barsh G.S.;
                                                                                                                                                                                                                                                                                                                                                        DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAF1_RAT
P54842;
                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Transcription factor MAF1 (Segmentation protein KR) (Kreisler).
MAFB OR MAFI OR KRML.
MAFB OR WASE)
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical 36.6 kDa protein in YPT52-DBP7 intergenic region.
                                                    Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 1; Length 322;
Pred. No. 2.6e+02;
0; Mismatches 2; Indels
 Histidine biosynthesis; Transferase; Glycosyltransferase;
                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                          Duesterhoeft A., Moestl D., Poehlmann R., Philipssen P., Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .l protein.
322 AA; 36647 MW; D7A601A46839244C CRC64;
                     08C14D1F6E98A31D CRC64;
                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                   Score 19; DB 1;
Pred. No. 2.5e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 AA.
                                                                                                                                                                        322 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=95094266; PubMed=8001130;
                     33821 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.5%;
66.7%;
                                                   90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z28247; CAA82094.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          S0001730; YKR022C.
                     303 AA;
                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                      S38091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
           Complete proteome. SEQUENCE 303 AA;
                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
                                                                                                                   287 EAGASS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 EAGSSS 124
                                                                                               1 eagxxs 6
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                                                                                                                                                                                                                                                                                                                 STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
SEQUENCE 32
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                                                                                                                                                                       YK02_YEAST
P36118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAF1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P54841;
                                                                                                                                                  RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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KW
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
zipper transcription factor.";

Cell 79:1025-1034(1994).

-1- FUNCTION: MAY PLAY AN EARLY ROLE IN AXIAL PATTERNING (HINDBRAIN SECMENDATION).

-1- SUBCELLULAR LOCATION: Nuclear.

-1- TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY, GUT, LUNG, AND BRAIN.

-1- DEVELOPMENTAL STAGE: DETECTABLE AT 8.0 DPC (ONE SOMITE) AS A BAND.

IN THE CAUDAL HINDBRAIN, AND BY 8.5 DPC (SIX TO EIGHT SOMITES),

THE HIGH LEVEL DOMAIN EXHIBITS A SHARP ROSTRAL EDGE COINCIDENT WITH THE R4/R5 BOUNDARY AND A DIFFUSE CAUDAL EDGE COINCIDENT THROUGH R6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-WISTAR; TISSUE-Liver;
MEDLINE=97190228; PubMed=9038383;
Sakai M., Imaki J., Yoshida K., Ogata A., Matsushima-Hibaya Y.,
Kuboki Y., Nishizawa M., Nishi S.;
"Rat maf related genes: specific expression in chondrocytes, lens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N->S: LOSS OF TRANSCRIPTIONAL ACTIVITY. D77AE07ABD9C2AD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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cocqee 14:745-750(1997).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE BZIP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                         INTOLOGY AND STATE BY THE BY TAMILY. MAR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 1; Length 323;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding; Nuclear POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASIC MOTIF.
LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L36435; AAA65689.1; -. HSSP; P05412; LJUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:104555; Mafb.
InterPro; IPR001871; bZIP.
Pfam; PF03131; bZIP_Maf; 1.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription factor MAF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264
287
248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
'-Loc 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248
323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T01439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 EAGSTS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 eagxxs 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAFB OR MAF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myristoylated alanine-rich C-kinase substrate (MARCKS) (Protein kinase c substrate, 80 kDa protein, light chain) (PKCSL) (80K-L protein).
MACS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE-9131795; Pubmed-1860846;
MEDILINE-91317795; Pubmed-1860846;
Harlan D.M., Graff J.M., Stumpo D.J., Eddy R.L. Jr., Shows T.B.,
Bayle J.M., Blackshear P.J.;
Gene (MACS).
Analysis of its gene product, promoter, and chromosomal J. Biol. Chem. 266:14399-14405(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                         Score 19; DB 1; Length 323; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                   DNA-binding; Nuclear protein
                                                                                                                                                                                                                                                                 6E386340D1F840A5 CRC64;
                                                                                                                                                                                                                                                     LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                          POLY-ALA.
BASIC MOTIF.
                                                                                                                                                                                                 POLY-HIS.
                                                                                                                                                                                                                                                                  35792 MW;
                                                                                                            EMBL; U56241; AAB50062.1; -. HSSP; P05412; 1JUN.
                                                                                                                                                                                                                                                                                                         90.5%;
                                                                                                                                      Interpro; IPR001871; bZIP.
Pfam; PF03131; bZIP_Maf; 1.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                   Transcription regulation;
                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                 323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                             158
194
238
266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                         308 EAGSTS 313
                                                                                                                                                                                                                                                                                                                                                                1 eagxxs 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MACS_HUMAN
P29966;
                                                                                                                                                                                                                        DOMAIN
DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
MACS_HUMAN
                                                                                                                                                                                                                                                                                                                                     Matches
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Neutral protease II precursor (EC 3.4.24.39) (Deuterolysin) (NPII).
Aspergillus oryzae.
                                                                                                                                                                                                                                     PHOSPHORILATION (BY PKC).
S -> A (IN REF. 1).
P -> S (IN REF. 1).
P -> S (IN REF. 1).
LVCPREGERAPREPAAAASS ->
IVCPREGERAPRESERAAAASS ->
IVCPREGESPREGARERELNO (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Fundi, Ascomycota, Pezizomycotina, Burotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 176-210; 279-281 AND 304-341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - PTM: PROBABLY POSSESSES THRRE DISULFIDE BONDS.
-! - SIMILARITY: BELONGS TO PEPTIDASE FAMILY M35 (ZINC
METALLOPROTEASE); ALSO KNOWN AS THE DEUTEROLYSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                              Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                            Length 331;
                                                                                                                                                                                                                                                                                                                                 Score 19; DB 1; Lengtn 332
Pred. No. 2.7e+02;
. --t-hes 2; Indels
                                                                                                                                                                 BY SIMILARITY.
MYRESTATE (BY SIMILARITY).
CALMODULIN-BINDING (PSD).
PHOSPHORYLATION (BY PKC).
                                                                                                                                                                                                                          (BY
(BY
                                                                                                                                                                                                                           PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 AA
          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                            PRINTS; PRO0963; MARCKS.
PROSITE; PS00826; MARCKS_1, 1.
PROSITE; PS00827; MARCKS_2; 1.
Phosphorylation; Myristate; Cal
                                                                                                                                                                                                                                                                                                          31413 MW;
                              EMBL; M68956; AAA59555.1; -. EMBL; M68955; AAA5954.1; -. EMBL; D10522; BAA01392.1; -. PIR; A38873; A38873. MIM; 177061; -.
                                                                                                                                                                                                                                                                                                                                            90.5%;
                                                                                      InterPro; IPR002101; MARCKS.
Pfam; PF02063; MARCKS; 1.
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                          331 AA;
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5062;
                                                                                                                                                                                          151
158
162
166
169
169
83
1118
233
                                                                                                                                                                                                                                                                                                                                                                                                             205 EAGAAS 210
                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                       1 eagxxs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPII_ASPOR
P46076;
                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                         Membrane.
INIT_MET
LIPID
                                                                                                                                                                                                                                       MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                         DOMAIN
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                            CONFLICT
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                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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П
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LEUB OR LEUC
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P41019;
                                                                                              TRANSMEM
TRANSMEM
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                                                                                                                                    TRANSMEM
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
LEU3_BACME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu Q., Dunlap J.C.; "Isolation and analysis of the arg-13 gene of Neurospora crassa."; Genetics 143:1163-1174(1996).
                                                                                                                                                                                                                                                                                   NEUTRAL PROTEASE II.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
070C5131335B7F44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1; Length 55.7
Pred. No. 2.9e+02;
                                                                                                                            InterPro; IPR001384; Peptidase_M35.
InterPro; IPR0001384; Peptidase_M35.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF02102; Peptidase_M35; 1.
PRINTS; PR00768; DEUTERCLYSIN.
Hydrolase; Mctalloprotease; 2inc; Signal; Zymogen.
SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96400914; PubMed=8807290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid transporter arg-13
                                                                                                                                                                                                                                                                                                                                                                                                                     90.5%;
66.7%;
                                                                                              EMBL; S53810; AAB19701.1; -.
                                                                                                                                                                                                                                                                                                                                                                  37517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                          304
307
352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                    176
303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 EAGSTS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 eagxxs 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR13_NEUCR
Q01356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BDA;
                                                                                                                                                                                                                                                                                                                            ACT_SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR13_NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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 δλ
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DD4CD
DD
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EMBL; L36378; AAC37500.1; -.

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01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)
(IMDH) (3-IPM-DH).
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                             ó
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0
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SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                   90.5%; Score 19; DB 1; Length 363; 66.7%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.5%; Score 19; DB 1; Length 367; 66.7%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS004/70; IDH_IMPH; 1.
Oxidoreductase; Leucine biosynthesis; NAD.
SEQUENCE 367 AA; 39942 MW; DC04D48E0EEABODD CRC64;
                                                                                                                                                          POTENTIAL.
8B87A937F6D37DC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 AA.
                                                                                                                                                                                                                                                                          Pred. No. 3e+(
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3e+C
0; Mismatches
                                                                                                                                       POTENTIAL.
                                                                                                             POTENTIAL
EMBL; AF279268; AAF87777.1; -.
INTERPO; IPR001993; Mitcoch_carrier.
Pfam; PF00153; mitco_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                 39401 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X65184; CAA46295.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S38506; S38506.
HSSP; P12010; 2AXQ.
InterPro; IPR001804; Isodh.
Pfam; PF00180; Isodh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                          334 3:
363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus megaterium.
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                      14 EAGAAS 19
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differentiation during late development of Dictyostellular dense Dev. 8:2086-2096(1994).

C. I- FUNCTION: RECEPTOR FOR CAMP. REGULATES AXIAL PATTERNING AND CELULAR DIFFERENTIATION DURING LATE DEVELOPMENT. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS.

C. I- SUBCELLULAR LOCATION: Integral membrane protein.

CONTINUES TO ACCUMULATE INTO CULAINATION.

CONTINUES TO ACCUMULATE INTO CULAINATION.

C. I- PTM: CARBOXXL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.

C. I- SIMILARITY: BELONGS TO FAMILY 5 OF G-PROTEIN COUPLED RECEPTORS.

B DICTYDD; DO07???; carD.

R InterPro: IPRO00848; GPCR.CAMP.

R InterPro: JPR000848; GPCR.CAMP.

R PRAMIS; PR000247; GPCRCAMP.
                                             Louis J.M., Ginsburg G.T., Kimmel A.R.;
"The cAMP receptor CAR4 regulates axial patterning and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (POTENTIAL).

(YTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                              PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
6-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Multigene family.
DOMAIN 11 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                          2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                           1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                MEDLINE=95047357; PubMed=7958880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.5%;
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343
412
443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
    SEQUENCE FROM 'N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 EAGSTS 77
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Q08103;
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TRANSMEM
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Hirata D., Fukui S., Yamashita I.;

Agric. Biol. Chem. 52:2647-2649(1988).

Agric. Biol. Chem. 52:2647-2649(1988).

-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY AI; ALSO KNOWN AS THE EURARYOTIC ASPARTYL PROTEASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycopsidaceae; Saccharomycopsis.
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Pred. No. 3.2e+02;
0; Mismatches 2; Indels
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3.2e+02;
.~~ 2; Indels
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350BF97116C54796 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Last annotation update)
                                                                                                        390 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; Pruvozu, Dr. Pruvozu, PRINTS; PROOTS2; PESSIN. PROSTITE; PSO0141; ASP_PROTEASE; 2. Hydrolase; Aspartyl protease; Signal. 18 POTEMILAL.
                                                                                                                                                                                   Acid protease precursor (EC 3.4.23.-).
                                                                                                                                                                                                                 Saccharomycopsis fibuligera (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JT0334; JT0334.
HSSP: P22329; JYPS.
InterPro: IPR001969; Asp_protease.
InterPro: IPR001461; Pepsin.
Pfam; PF00026; asp; 1.
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16-OCT-2001 (Rel. 40, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41263 MW;
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                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 AA;
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                                                                                                                                                                                                                                                                  NCBI_TaxID=4944;
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P22929;
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ACT_SITE
SEQUENCE
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                              48
                                                                                        CARP_SACFI
 Matches
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                                                                                                                                                                                                             ö
                                                                                                                                                                  Length 443;
                                                                                                                                                                                                           2; Indels
                                                                                                       CDF3A9DEE5A5BBE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                Score 19; DB 1; Pred. No. 3.6e+02; 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Glycoprotein GX precursor.
                                                                                                                                                                                                                                                                                                                                                                                                   444 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine herpesvirus type 1.2 (strain ST).
ASN-RICH.
POLY-ASN.
POLY-GLN.
                                                              POLY-GLN
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98295987; pubmed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Ebjlmeder K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole genome comparison of Mycobacterium tuberculosis clinical and
unique region (US) of the bovine herpesvirus type 1 (ST strain)."; Virology 199:409-421(1994).
                                                                                                                                                                                                                                            N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                            Length 444;
                                                                                                                                                                                                                                                                                                                         Score 19; DB 1; Length 444
Pred. No. 3.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laboratory strains.";
submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-- *MILLARIY: BELONGS TO THE UPF0089 FAMILY.
                                                                                                                                                                                                                                                                                   0145942AA35B05CB CRC64;
                                                                                                                                                                                     Glycoprotein; Transmembrane; Signal.
SIGNAL 1 24 POTENTIAL.
CHAIN 25 444 GLYCOPROTEIN GX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
116-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 50.9 kDa protein Rv3088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474 AA
                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                               EMBL; Z23068; CAA80603.1; -.
InterPro; IPR003363; Herpes_gG.
Pfam; PF02400; Herpes_gG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RV3088 OR MT3173 OR MTV013.09.
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                                                                                                                                                                                                                                                                                                                           90.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                   46708
                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                              390 4
117 1
240 2
335 3
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                        267 EAGSAS 272
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053305;
                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Surin B.P., Watson J.M., Hamilton W.D.O., Economou A., Downie J.A.;
"Molecular characterization of the nodulation gene, nodT, from two
blovars of Rhizobium leguminosarum.";
Mol. Microbiol. 4:245-252(1990).
-!- SUBCEDLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid sym pRL1JI.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                     Tuberculist; Rv3088; -.
Tuberculist; Rv3088; -.
InterPro: IPR004255; UPF0089.
Pfam; PF03007; UPF0089; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 474 AA; 50886 MW; 36832D972BE3851A CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nodulation protein T precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.58;
66.78;
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PIR; S10133; S10133.
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Best Local Similarity
'-has 4; Conserve
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                                                                                                                                                                                                                                                                                                                 TIGR; MT3173;
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ID NODT_RHILV
AC P15727;
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Pfam; PF00096; zf-C2H2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kageyama R., Sasal Y., Nakanishi S.;
"Molecular characterization of transcription factors that bind to the CAMP responsive region of the substance P precursor gene. CDNA cloning of a novel C/EBP-related factor.";
J. Biol. Chem. 266:15525-15531(1991).
-!- FUNCTION: A TRANSCRIPTIONAL ACTIVATOR, PROBABLY CONSTITUTIVE, WHICH BINDS TO THE CAMP RESPONSIVE REGION (CRE) (CONSENSUS: 5'GTGAGCT(A/C)(A/G)-3'); A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS.
-!- SHDNDS DAMA AS A DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                  000969; Q62870;
01-ARR-1993 (Rel. 25, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cyclic-AMP-dependent transcription factor ATF-2 (Activating transcription factor 2) (cAMP response element binding protein CRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Nuclear.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- SIMILARITY: BELONGS TO THE BZIP FAMILY. ATF SUBFAMILY.
                                                                                                                                                                   ;
0
                                          POTENTIÁL.
NODULATION PROTEIN T.
N-ACYL DIGLYCERIDE (POTENTIAL).
DSSSB46566E54R82 CRC64;
                                                                                                                                        Length 482;
                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     Score 19; DB 1;
Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                         487 AA.
                                                                                                                                                                   0; Mismatches
            Pfam; PF02321; OEP; 2.
Plasmid; Nodulation; Lipoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91332085; PubMed-1714459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A39429; A39429.
HSSP, P08047; 1SP2.
TRANSFAC; T01382; -
InterPro; IPR000822; Znf-C2H2.
InterPro; IPR001871; bZIP.
                                                                                         51488 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U38938; AAA93263.1; -. EMBL; M65148; AAA42013.1; -.
                                                                                                                                   90.5%;
                                                                                                                                                                   4; Conservative
InterPro; IPR003423; OEP
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00170; bZIP; 1.
                                                                                       482 AA;
                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                             201 EAGAAS 206
                                                                                                                                                                                                1 eagxxs 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muramatsu S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                         SEQUENCE
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                       ATF2 RAT
                                            SIGNAL
                                                            CHAIN
                                                                          LIPID
                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLASMAG 30:30123-308(1993).

-!- FUNCTION: RESISTANCE TO HG(2+) IN BACTERIA APPEARS TO BE GOVERNED BY A SPECIALIZED SYSTEM WHICH INCLUDES MERCURIC REDUCTASE. MERA PROTEIN IS RESPONSIBLE FOR VOLATILIZING MERCURY AS HG(0).

-!- CATALYTIC ACTIVITY: Hg + NADP(+) + H(+) = Hg(2+) + NADPH.

-!- COPACTOR: FAD.

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
                                                                                                                                                                                                                                                                                                                                  Gaps
transposable element from an environmental Acinetobacter strain."; Plasmid 30:303-308(1993).
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94134837; PubMed-8302940;
Kholodii G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin S.Z.,
Yuriava O.V., Nikiforov V.G.;
"Molecular characterization of an aberrant mercury resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
                                                                                                                                                                                                                                                                                                 Length 487;
                                                                                                                                                                        PHOSPHORYLATION (BY MAPK14)
                                                                                                                                                                                                      PHOSPHORYLATION (BY MAPK14)
                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                   SIMILARITY).
MISSING (IN ISOFORM 2).
4ED95B106DF5F9EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mercuric reductase (EC 1.16.1.1) (Hg(II) reductase).
                                                                                                                                                                                                                                                                                                  DB 1;
4e+02;
                                                                                                                                       BASIC MOTIF.
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              561 AA.
                                                                                                                                                                                                                                                                                                                 Pred. No. 4e+(); Mismatches
                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                  Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 HMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001934; HMA.
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                                                                                                                                                                                                                                                    52286 MW;
                                                                                                                                                                                                                                                                                                 90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OXIDOREDUCTASES CLASS-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acinetobacter calcoaceticus.
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                          31
356
390
                                                                                                                                                                        51
                                                                                                                                                                                                                                                 487 AA;
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                                               452 EAGATS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pKLH2.
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DOMAIN
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AC22_STRCO
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-1- FUNCTION: RESISTANCE TO HG(2+) IN BACTERIA APPEARS TO BE GOVERNED BY A SPECIALIZED SYSTEM WHICH INCLUDES MERCHRIC REDUCTASE. MERA PROTEIN IS RESPONSIBLE FOR VOLATILIZING MERCHRY AS HG(0).

-1- CATALYTIC ACTIVITY: Hg + NADP(+) + H(+) = Hg(2+) + NADPH.

-1- COFACTOR: FAD.

-1- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.

-1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE

OXIDOREDUCTASES CLASS-I.
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pKLH272.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97303088; PubMed=9159519; Virieva O., Kholodii G., Minakhin L., Gorlenko Z., Kalyaeva E., Mindlin S., Nikiforov V.; Intercontinental spread of promiscuous mercury-resistance
                                                                                                                                                                                                                                                   FAD (FLAVIN PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                           Pfam; PF00013; MAA; 1.
Pfam; PF00013; MAA; 1.
Pfam; PF00013; MAA; 1.
Prints, PR00369; FADPR.
PRINTS; PR00369; FADPR.
PRINTS; PR00945; HGRDTASE.
PROSTTE; PS01047; HMA_1; 1.
PROSTTE; PS01047; HMA_2; 1.
PROSTTE; PS00076; PRIDINE_REDOX_1; 1.
PROSTTE; PS50846; HMA_2; 1.
PROSTTE; PS50846; PMA_2; 1.
PROSTTE; PS50846; PMA_2; 1.
PROSTTE; PS00076; PRIDINE_REDOX_1; 1.
MACCULY; Redox_active_center; Metal-binding; Plasmid.
                                                                                                                                                                                                                                                                                                                                     Score 19; DB 1; Length 561;
Pred. No. 4.6e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                         (ADP PART) (PROBABLE).
                                                                                                                                                                                                                                                                HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
111E02A702C157D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mercuric reductase (EC 1.16.1.1) (Hg(II) reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacter agglomerans (Pantoea agglomerans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                561 AA
                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                        FAD (ADP PART REDOX-ACTIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transposons in environmental bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 HMA DOMAIN.
InterPro; IPR000815; Hg_reductase.
InterPro; IPR001100; pyr_redox.
InterPro; IPR004099; pyr_redox_dim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                              58558 MW;
                                                                                                                                                                                                                                                                                                                                      90.5%;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                            561 AA;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=549;
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                                                                                                                                                                                                                                                                                                                                                                                             1 eagxxs 6
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P94702;
                                                                                                                                                                                                                      NP_BIND
DISULFID
                                                                                                                                                                                                                                                   NP_BIND
METAL
                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                            DOMAIN
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MERA_ENTAG
                                                                                                                                                                                                                                                                                                                                                                                                                          45
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the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2);
Warren T., Harris D., Cerdeno A.M., Parkhill J., Barrell B.G.,
Rajandream M.A.:
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROMOTES THE EFFLUX OF ACTINORHODIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- STMLARITY: BELONGS TO THE MAJOR PACILITATOR FAMILY (ALSO KNOWN
AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fernandez-Moreno M.A., Caballero J.L., Hopwood D.A., Malpartida F., "The act cluster contains regulatory and antibiotic export genes, direct targets for translational control by the blda tRNA gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1902;
                                   R HASP; QUADDS; LAWO.

R HASP; QUADDS; LAWO.

R InterPro; IPR001934; HWA.

InterPro; IPR001934; HWA.

R InterPro; IPR000205; NAD_binding.

R InterPro; IPR00409; Pyr_redox.

InterPro; IPR00409; pyr_redox.

R Pfam; PF00870; Pyr_redox. 1.

R Pfam; PF00852; pyr_redox. 1.

R Pfam; PF00855; hRAPTASE.

R PRIMTS; PR00945; HRAPTASE.

R PRIMTS; PR00941; PNDRDTASE.

R PROSITE; PS00104; HWA_1; 1.

R PROSITE; PS00076; PYRIDINE_REDOX_1; 1.

R PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               FAD (FLAVIN PART) (BY SIMILARITY).
HG(2+) (POTENTIAL).
HG(3+) (POTENTIAL).
FABAO7D7ECZF13C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.5%; Score 19; DB 1; Length 561; 66.7%; Pred. No. 4.6e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        FAD (ADP PART) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                    center; Metal-binding; Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
Probable actinorhodin transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       578 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              REDOX-ACTIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MΨ.
EMBL; Y08992; CAA70184.1; -.
HSSP; Q04656; 1AW0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTII-2 OR SCBAC28G1.09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                               403
558
559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces.";
Cell 66:769-780(1991).
                                                                                                                                                                                                                                                                                                                                                                       Mercury; Redox-active
                                                                                                                                                                                                                                                                                                                                                                                                                            136
393
558
559
561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 eagxxs 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC22_STRCO
P46105;
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NP_BIND
METAL
                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
NP_BIND
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MEDLINE=90375493; PubMed=2118903;
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                     EMBL; M57518; AAA27287.1; -. EMBL; D63999; BAA10059.1; -.
                                                                                                                                                                                                                                                                                                                             90.5%;
                                                                                               InterPro; IPR001023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opportunistic pathogen."; Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa,
                                                             C39025; C39025.
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                P04475; 1DG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                    615 EAGTSS 620
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ETA OR PA1148.
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                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 19
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  and for commercial
                   (See http://www.isb-sib.ch/announce/
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chaperone protein darK2 (Heat shock protein 70-2) (Heat shock 70 kDaprotein 2) (HSP70-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-96127529; DubMed-8590279;
MEDLINE-96127529; DubMed-8590279;
MEDLINE-96127529; DubMed-8590279;
Sugiura M., Tabata S.;
Sugiura M., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.;
Sug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDIINE-91093185; PubMed-1670771;
CLittnis P.R., Melson N.;
"Molecular cloning of the genes encoding two chaperone proteins of the cyanobacterium Synechocystis sp. PCC 6803.";
J. Biol. Chem. 266:58-65(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 1; Length 578;
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0; Mismatches 2; Indels
  Usage by
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Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                           modified and this statement is not removed.
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                   entities requires a license agreement (Sor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                 232
259
306
341
369
444
546
578 AA;
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P22358;
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SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDLINE=2043737; Pubmed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Alckey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-84194063; PubMed-6201861; Gray G.L., Smith D.H., Baldridge J.S., Harkins R.N., Vasil M.L., Chen E.Y., Heyneker H.L.; and expression in Escherichia coli of the exotoxin A structural gene of Pseudomonas aeruginosa."; Proc. Natl. Acad. Sci. U.S.A. 81:2645-2649(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOXA_PSEAE STANDARD; PRT; 638 AA.
P11439; Q91417;
01-00T-1989 (Rel. 12, Created)
16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Rel. 40, Last annotation update)
Exotoxin A precursor (NAD-dependent ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                      Length 636;
                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 1; Length 636
Pred. No. 5.2e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                636 AA; 67614 MW; 33AE4CECBA28F40A CRC64;
PRINTS; PR00301; HEATSHOCK70.
PR051TE; PS001297; HSP70_1; 1.
PROSITE; PS00139; HSP70_2; 1.
PROSITE; PS00136; HSP70_2; 1.
Chaperone; ATP-binding; Heat shock; Multigene family; EQUENCE 636 A5, 67614 MW; 33AE4CECBA28F40A CRC64
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384 EAGAAS 389
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SGT1_ARATH
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III (REQUIRED FOR ADP-RIBSOSYL ACTIVITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXOTOXIN A.

II (REQUIRED FOR TARGET CELL
RECGGNITION).

II (REQUIRED FOR TRANSLOCATION IN TARGET
CELL CYTOPLASM).
                                                                                                                                                           Li M., Dyda F., Benhar I., Pastan I., Davies D.R.; "The crystal structure of Pseudomonas aeruginosa exotoxin domain III with nicotinamide and AMP: conformational differences with the intact
                                                                                                                                                                                                                                                                "Crystal structure of the catalytic domain of Pseudomonas exotoxin A complexed with a nicotinamide adenine dinuclectide analog:
"Crystal structure of the catalytic domain of Pseudomonas exotoxin A complexed with a nicotinamide adenine dinuclectide analog:
"Implications for the activation process and for ADP ribosylation.";
Proc. Natl. Acad. Sci. U.S.A. 93:6902-6906(1996).

I- CHUCTION: THIS TOXIN IS AN NAD-DEPENDENT ADP-RIBOSYLENSFERSE.
IT CAPALYZES THE TRANSFER OF THE ADP RIBOSYL MOIETY OF OXIDIZED NAD ONTO ELONGATION FACTOR 2 (EF-2) THUS ARRESTING PROTEIN
                                                               Bourdenet S., Vacheron M.-J., Guinand M., Michel G., Arminjon F.; "Biochemical and immunochemical studies of proteolytic fragments of exotoxin A from Pseudomonas aeruginosa.";
                                                                                                                                                                                                                                                                                                                                                                       SYNTHESIS.
PTM: THE 8 CYSTEINES PARTICIPATE IN INTRACHAIN DISULFIDE BONDS.
SIMILARITY: REGIONAL SEQUENCE SIMILARITY AT THE ACTIVE SITE
WITH DIPHTHERIA TOXIN (DT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; JAER; 10-JUN-96.
PDB; JDMA; 15-SEP-95.
Toxin; Signal; Transferase; Glycosyltransferase; NAD; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> N (IN REF. 1).
-> V (IN REF. 1).
-> S (IN REF. 1).
7B9AAD56A27C700A CRC64;
                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 92:9308-9312(1995).
                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 424-638.
MEDLINE=96293446; Pubmed=8692916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IN REF. 1).
(IN REF. 1).
(IN REF. 1).
                                                                                                                                   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 424-638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACT WITH NAD
responsible for the animal toxicity.";
J. Biol. Chem. 265:16306-16310(1990).
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                                                                                                         Eur. J. Biochem. 192:379-385(1990).
                                                                                                                                                MEDLINE=96016159; PubMed=7568123;
                                                   MEDLINE=91006124; PubMed=2170123;
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EMBL; AE004544; AAG04537.1; -.
PIR; A30347; A30347.
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277
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204
389
432
540
638 AA;
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Matches 4; Conserv
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578
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Ryan K., Garrett N., Mitchell A., Gurdon J.B.;
"Eomesodermin, a key early gene in Xenopus mesoderm differentiation.";
Cell 87:989-1000(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell 87:989-LUUU(1996).
-!- FUNCTION: INVOLVED IN MESODERM DIFFERENTIATION. ACTIVATES WNT8,
BRACHYURY, CHD MIX.1 EXPRESSION.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- DEVELOPMENTAL STAGE: FIRST EXPRESSED AT OR JUST AFTER MIDBLASTULA
                                                                                                                    SGTI protein homolog At5g65490.
AT5G65490 OR K1904.2.
Arabidopsis thaliama (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Kaneko I., Katoh I., Asamizu E., Sato S., Nakamura Y., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SGT1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 5.3e+02;
0; Mismatches 2; Indels
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643 AA; 73161 MW; 9F9DD990F65B4C4F CRC64;
                                            01-WAR-2002 (Rel. 41, Created)
01-WAR-2002 (Rel. 41, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
01-MAR-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB026638; BAA98169.1; -.
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Best Local Similarity
'-hac 4; Conserva
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    SGT1_ARATH Q9LSM5;
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Gaps

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DB 1; Length 638;

Score 19; DB 1; Length 638 Pred. No. 5.3e+02; Mismatches 2; Indels

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Conservative

9 eagxxs

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90.5%;

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DOMAIN
DOMAIN
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MEDLLINE-97432816; PubMed-9286696;
Rauch U., Meyer H., Brakebusch C., Seidenbecher C., Gundelfinger E.D.,
Beier D.R., Fassler R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i TISSUE SPECIFICITY: BRAIN (BY SIMILARITY).
-i PTW: CONTAINS MOSTLY CHONDROITH SULFATE (BY SIMILARITY).
-i- SIMILARITY: CONTAINS 1 INMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-i- SIMILARITY: CONTAINS 2 LINK DOMAINS.
-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 1 GF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 1 STORY (SCR) DOMAIN.
-i- SIMILARITY: CONTAINS 1 STORY (SCR) DOMAIN.
-i- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00907; T-box.
Pfam; PF00907; T-box. 1.
PROM917; PR001937; T-Box. 1.
PROSITE; PS01283; TBOX. 1.
PROSITE; PS01284; TBOX. 2; 1.
PROSITE; PS01284; TBOX. 2; 1.
PROSITE; PS01284; TBOX. 3; 1.
PROSITE; PS01284; TEOX. 3; 1.
PROSITE; PS01284; PS01285; PS012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 1; Length 692;
Pred. No. 5.7e+02;
0; Mismatches 2; Indels
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; 9D129A67F6357989 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                SIMILARITY: CONTAINS 1 T-BOX DOMAIN.
                                                                                                                    DOMAIN: CONTAINS 13 S-P-X-X REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 443 T.
692 AA; 75943 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U75996; AAC60061.1; -. HSSP; P24781; 1XBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.5%;
                                                                                      INDUCTION: BY ACTIVIN.
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Best Local Similarity
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N-LINKED (GLCNAC. .) (POTENTIAL).
CC2C33C97B453E45 CRC64;
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SUSHI.
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InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
Pfam; PF00008; EGF; 1.
Pfam; PF000047; ig; 1.
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InterPro; IPR000742; EGF_2.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                    EMBL; X87096; CAA60575.1; -. HSSP; P20693; 1HLJ.
                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; 19; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
ProDom; PD000918; Link; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 1.
SMART; SM00406; IGV; 1.
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336
883 AA;
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DOMAIN
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STRAIN-SPRAGUE-TAWLEY. TISSUE-Brain;

MEDLINE-94216386; PubMed=7512973;

MAY PLAY A ROLE IN THE TERNINALLY DIFFERENTIATING AND THE ADULT NEXVOUS SYSTEM DUBING POSTNATAL DEVELOPMENT. COULD THE ADULT NEXVOUS SYSTEM DAY FUNCTION AS A CHONDROITIN SULFATE-COULD THE MEMBRANE BY A CHONDROITIN SULFATE-COULD SURFACE RECEPTOR.

MATACHED TO THE MEMBRANE BY A SECRETED FORM (SHOWN HERE) AND A GPI-ANCHORED FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

MATACHED TO THE MEMBRANE BY A SECRETED FORM (SHOWN HERE) AND A GPI-ANCHORED ISOFORM INCREASES AFTER DAY PR.

MATACHED MOSTLY CHONDROITIN SULFATE.

MATACHED MOSTLY CHONDROITIN SULFATE.

MELARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TIPE DOMAIN.

MELARITY: CONTAINS 1 EGF-LIKE DOMAIN.

MELARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.

MELARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.

MELARITY: CONTAINS 1 SULFANNI SERVICE NOWENCED FORM MERCHANDER FORM MER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 364 ONWARD AND IS SMALLER (371 AA) DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                "Brevican, a chondroitin sulfate proteoglycan of rat brain, occurs as secreted and cell surface glycosylphosphatidylinositol-anchored isoforms.";
                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=96074575; PubMed=7488217;
Xamada H., Watanabe K., Shimonaka M., Yamasaki M., Yamaguchi Y.;
"CDNA cloning and the identification of an aggrecanase-like cleavage site in rat brevican.";
                                PGCB_RAT STANDARD; PRT; 883 AA.
P55068; 063040; 062860; 063513;
01-0CT-1996 (Rel. 34, Created)
10-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Brevican core protein precursor (Brain enriched hyaluronan binding protein) (BEHAB protein).
                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
BODILNE-SP6070828; PubMed=7592978;
Seidenbe-ber C.I., Richter K., Rauch U., Faessler R., Garner C.C.,
Gundelfinger E.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 216:957-963(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 396-407.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 270:27206-27212(1995).
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EMBL; X86406; CAA60160.1; -.
EMBL; U37142; AAA87847.1; -.
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EAD EACH LA.

C-TYPE LLC.
C-TYPE LLC.
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C-TYPE LLC.
SUSHI.

B SIMILARITY.

J 321 BY SIMILARITY.

J 47 BY SIMILARITY.

J 52 BY SIMILARITY.

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Pred. No. 7.38+02;
0; Mismatches 2; Indels
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LINK 2.
EGF-LIKE.
C-TYPE LECTIN.
SUSHI.
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EMBL; Z28366; CAA82215.1; ALT_FRAME.
HSSP; P20693; 1HLJ.
                                                                                                                                                                                                                                      InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
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InterPro; IPR000742; EGF_2.
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Ig_MHC.
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66.7%;
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Link.
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                                                                                                                                                            InterPro; IPR003006;
InterPro; IPR003596;
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Best Local Similarity
Matches 4; Conserv
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RESULT 24 SRCA\_RABIT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: SECHENT A ENCODES A POLYPROTEIN, THAT IS PROCESSED INTO THE MAJOR STRUCTURAL PROTEINS OF THE VIRION VP2 AND VP3, AND INTO THE PUTATIVE PROTEASE VP4.
                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE OF 703-1012 FROM N.A.
MEDLINE=86220784; PubMed=3011501;
Hudson P.J., McKern N.M., Fahey K.J., Azad A.A.;
"Predicted sequence of the host-protective immunogen of infectious bursal disease virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Thiazide-sensitive sodium-chloride cotransporter (NA-CL symporter).
SLC12A3 OR TSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polyprotein; Structural protein; Nonstructural protein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NONSTRUCTURAL PROTEIN VP4 (PROTEASE).
MINOR STRUCTURAL PROTEIN VP3.
M; D9320A90459DE8F6 CRC64;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=86259073; PubMed=3014441;
Hudson P.J., McKern N.M., Power B.E., Azad A.A.;
"Genomic structure of the large RNA segment of infectious bursal
                                                                                                       Structural polyprotein (Contains: Major structural protein VP2; Nonstructural protein VP3]. Avian infectious bursal disease virus (strain Australian 002-73)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAJOR STRUCTURAL PROTEIN VP2.
                                                                                                                                                                                           dsRNA viruses; Birnaviridae; Avibirnavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 1; 1
Pred. No. 8.4e+02;
0; Mismatches 2;
                                       01-AUG-1988 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 14:5001-5012(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X03993; CAA27629.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002662; Birna_VP2.
InterPro; IPR002663; Birna_VP3.
InterPro; IPR002664; Birna_VP4.
Pfam; PF01766; Birna_VP2; 1.
Pfam; PF01767; Birna_VP3; 1.
Pfam; PF01768; Birna_VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 201:143-146(1986).
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1012 AA; 109503
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  STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                 NCBI_TaxID=10997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S50.002;
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P55017;
  POLS_IBDVA
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TSCC_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and expression of cDNA encoding the 53,000-dalton glycoprotein of rabbit skeletal muscle sarcoplasmic reticulum.";
J. Biol. Chem. 264:3484-3493(1989).
I- FUNCTION: PERHARS INVOLYED IN THE REGULATION OF CALCIUM TRANSPORT.
I- SUBCELLULIAR LOCATION: SARCOPLASMIC RETICULUM LUMEN. ASSOCIATED THROUGH CA(2+) WITH THE MEMBRANE.
I- ALTERNATIVE PRODUCTS. 2 ISOFORMS; A CALCIUM-BINDING CLYCOPROTEIN/160 KDA (SHOWN HERE) AND A SECOND GLYCOPROTEIN/53 KDA; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89123480; PubMed-2521635;
Leberer E., Charuk J.H.M., Clarke D.M., Green N.M., Zubrycka-Gaarn E.,
McLennan D.H.;
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89345602; PubMed-2762314; Leberer E., Charuk J.H.M., Green N.M., Maclennan D.H.; Molecular cloning and expression of cDNA encoding a lumenal calcium binding glycoprotein from sarcoplasmic reticulum."; Proc. Natl. Acad. Sci. U.S.A. 86:6047-6051(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 KDA SARCALUMENTN.
ACIDIC DOMAIN, PROBABLY BINDS CALCIUM.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN 53 KDA ISOFORM).
                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A48CAA221AE1418B CRC64;
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                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
116-CCT-2001 (Rel. 40, Last annotation update)
Sarcalumenin precursor.
                                                                                                       908 AA.
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PIR; A33280; A33280.
PIR; A33312; A33312.
                                                                                                       STANDARD;
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908 AA;
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558 EAGSSS
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P13666;
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Gaps

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2; Indels

Length 1012;

DOMAIN CARBOHYD

CHAIN

SIGNAL CHAIN CARBOHYD

VARSPLIC CONFLICT SEQUENCE

Query Match

Best Loc Matches

RESULT 25 POLS\_IBDVA

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121
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ISWI_DROME
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                                                                                                                                                                                                  Mastroianni N., de Fusco M., 20110 M., Arrigo G., Zuffardi O.,
Mastroianni N., de Fusco M., 20110 M., Arrigo G., Zuffardi O.,
Mettinelli A., Ballabio A., Casari G.;
"Molecular cloning, expression pattern, and chromosomal localization
of the human Na-c1 thiazide-sensitive cotransporter (SLC12A3).";
Genomics 35:486-493(1996).

C. PUNCTION: ELECTRACALLY SILENT TRANSPORTER SYSTEM WHICH IS A
MEDIATOR OF SODIUM AND INTEGRAS OFFICIAL.

C. SUBCELLULAR LOCATION: Integral membrane protein.

C. SUBCELLULAR LOCATION: Integral membrane protein.

C. TISSUE SPECIFICITY: PREDOMINANT IN KIDNEY.

C. INTEGRAL SECIPLOSIS OF GITELMAN'S SYNDROME

(SS), AN AUTOSOMAL RECESSIVE DISEASE CHARACTERIZED BY DIVERSE
ABNORMALITIES IN ELECTROLYTE HOMEOSTASIS INCLUDING HYPOKALAEMIC
METABOLIC ALKALOSIS. GS IS A SUBSET OF BARTIER'S SYNDROME.

C. SIMILARITY: BELONGS TO THE SIC12A FAMILY OF TRANSPORTERS.
                                             SEQUENCE FROM N.A., AND VARIANTS GS.

MEDLINE=96122035; PubMed=8528245;
Simon D.B., Nelson-Williams C., Bla M.J., Ellison D., Karet F.E.,
Molina A.M., Vaara I., Iwata F., Cushner H.M., Koolen M., Gainza F.J.,
Gitelman H.J., Lifton R.P.;
"Gitelman's variant of Bartter's syndrome, inherited hypokalaemic
alkalosis, is caused by mutations in the thiazide-sensitive Na-Cl
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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InterPro; IPR002948; NaCl_transporter.
PRINTS; PR01230; NACLTRNSPORT.
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                                                                                                                                                                             TISSUE=Kidney;
MEDLINE=97001149; PubMed=8812482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U44128; AAC50355.1; -. EMBL; X91220; CAA62613.1; -.
                                                                                                                                        Nat. Genet. 12:24-30(1996).
                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                   cotransporter.
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ISWI_DROWE STANDARD; PRT; 1027 AA.

Q24368; Q9V6E8;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
Iswi protein (Imitation swi protein) (Nucleosome remodeling factor 140 kDa subunit) (NURF-140) (CHRAC 140 kDa subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elfring L.K., Deuring R., McCallum C.M., Peterson C.L., Tamkun J.W., "Identification and characterization of Drosophila relatives of the yeast transcriptional activator SNF2/SWI2."; Mol. Cell. Biol. 14:225-2234(1994).
. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRALN-BEBEKELEN;
MEDILINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1021;
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Pred. No. 8.5e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG -> VV (IN REF. 2).
E -> D (IN REF. 2).
V -> GARPSVSGAL (IN REF. 1).
WW: D7ECE53DA6233821 CRC64;
                                                                                                                                                                                                                         A -> V (IN GS).
/FTIG=VAR_007119.
/FTIG=VAR_007120.
R -> H (IN GS).
/FTIG=VAR_007121.
R -> L (IN GS).
/FTIG=VAR_007121.
                                                                   P -> L (IN GS).

FTId=VAR_007114.

C -> R (IN GS).

/FTId=VAR_007115.

D -> N (IN GS).

P -> N (IN GS).

G -> C (IN GS).

/FTId=VAR_007116.
                                                                                                                                                                                                                                                                                                                                                        A -> T (IN GS).
/FTIG=VAR_007123.
G -> R (IN GS).
/FTIG=VAR_007124.
 N-LINKED (GLCNAC.
                                                                                                                                                                                            (IN GS).
R_007118.
                                                                                                                                                                                                                                                                                                                                                                   007123.
                                             /FTId=VAR_007113
P -> L (IN GS).
                                                                                                                                                                                                                                                                                                                                                                                                                        L -> P (IN GS).
/FTId=VAR_007125.
R -> Q (IN GS).
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                              M (IN
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                                                                                                                                                                                              MISSING
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MEDLINE=94187693; PubMed=7908117;
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 406
426
209
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766
807
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Best Local Similarity
`.hos 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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1021
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ATP (POTENTIAL).

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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
RA George R.A., Lowaris S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H.C., Blazel, R.G., Champe M., Pieliffer B.D.,
RA Abrill J.E., Agbayania A., Dan H.-J., Andrews-Pfrannkoch C., Baldwin D.,
Ballew R.M., Basu A., Paszendale J., Bahadaria D., Boslahakov S.,
Ballew R.M., Basu A., Daware B.P., Bhandaria D., Boslahakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Butler K.D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Butler K.D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Butli J.F., Agbayania A.D., Day Z., Chang P., Bortlers P.,
Bortler B., Delcher A., Deng Z., Mays A.D., Daw I., Dietz S.M.,
Budons K., Doug L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
Butlis K.J., Evangelista C.C., Ferrisca S., Plaischmann M.,
RA Hostin D., Houstra C.D., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalai M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalai M., Kalush F., Karpen G. H., Ke Z., Kannison D., Lai Z.,
Jalai M., Matteil R.D., Mouris J., Month J., Dietz S.,
Barko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Hostin N., Patten G. D., Karpen G. H., Ke Z., Kannison D.,
Reklow G., Milshina N.V., Mobarry C., Morris J., Morsken D.,
Reklow M., Pittman G.S., Pan M., Shapski M.P., Santh H., Shie S.,
Shie B.C., Siden-Kiamog I., Simpson M., Stupski M.P., Santh H., Shie S.,
Rahazoolo M., Pittman G.S., Pan S.,
Pollar C., Siden-Kiamog T., Simpson M., Stupski M.P., Shie H.,
Syliskas R., Woers E.W., Welley K., Wenter E.W., Welssen D.G., Shan M., Shang S.,
R. Honger S., Patter S., Welley M., Shon W., Santh H.,
R. Hang Z.Y., Weaserman D.A., Welley K., Welley S.,
R. Honger E.W., Worte
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CHROMATIN-REMODELING MACHINES.
-!- SUBUNIT: NURF IS COMPOSED OF FOUR SUBUNITS; A 215 KDA PROTEIN, INTEATION SWITCH (ISWI), NURF-55, AND NURF-38.
-!- SUBCELLULAR LOCATION: NUClear (Potential).
-!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY. SNF2L

SUBFAMILY.

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Nuclear protein; Helicase; ATP-binding. EMBL; AE003821; AAF58479.1; -. FlyBase; FBgn0011604; ISWi. InterPro: IPR001410; DEAD. InterPro: IPR0014010; Myb\_DNA\_bind. InterPro: IPR001005; Myb\_DNA\_bind. InterPro: IPR000330; SNF2\_N. IPR00176; SNF2\_N. IPR0WIT: SW00487; DEXDC: IPR0WIT: SW00487; DEXDC: IPROWERT: SW00489; DEXDC: IPROWERT: IPROWERT: SW00489; DEXDC: IPROWERT: IPROWERT: SW00489; DEXDC: IPROWERT: IPRO EMBL; L27127; AAA19868.1; -. SMART; SM00395; SANT;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MICROBIOLOGY 143:3877-3888(1997).

-1- FUNCTION: THE PLASMA MEMBRANE ATPASE IS A HYDROGEN ION PUMP. THE PROTON GRADIENT IT GENERATES DRIVES THE ACTIVE TRANSPORT OF NUTRIENTS BY H+- SYMPORT. THE RESULTING EXPERNAL ACIDIFICATION AND/OR INTERNAL ALKINIZATION MAY MEDIATE GROWTH RESPONSES.

-1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(IN) = ADP + PHOSPHATE +
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00122; E1-E2_ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
PRINTS; PR00120; HATPASE.
PROSITE; PS00154; ATPASE_E1_E2; 1.
Hydrolase; Hydrogen ion transport; Transmembrane; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                              Probable plasma membrane ATPase (EC 3.6.3.6) (Proton pump) (PAT2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98083743; pubMed=9421912;
Coukell M.B., Moniakis J., Cameron A.M.;
"The patB gene of Dictyostellum discoideum encodes a P-type H(+)-ATPase isoform essential for growth and development under acidic
                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IIIA.
                                                                                                               Score 19; DB 1; Length 1027;
Pred. No. 8.5e+02;
0; Mismatches 2; Indels
                                                 POLY-LYS.
W; 008FC81AE15E071F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPA

                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                               PRT; 1058 AA.
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                                   POLY-LYS.
                  DEAH BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictybb, DD00061; patb.
InterPro; IPR004014; Cation_ATPase.
InterPro; IPR001055; HarPase.
InterPro; IPR001055; HarPase.
InterPro; IPR001454; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00690; Cation_ATPase_N; 1.
                                                                  MW;
                                                                                                               90.58;
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                                                                 118873
                                                                                                                                                 4; Conservative
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160
259
981
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                                                                  AA;
                                                                                                                                  Best Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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P54679;
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SEQUENCE
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NP_BIND
SITE
                                DOMAIN
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                                                                                                                                                                                                                                                                RESULT 28
PMA1_DICDI
 FFF
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Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Mayer K.F.X., Schueller C., Wambutt R., Bridan K.-D., Terryn N.,
Mayer B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Metchert B., Portetalle D., Perez-Alonso M., Schmidthehni T.,
Marchert B., Portetalle D., Perez-Alonso M., Bornidthehni T.,
Langham S.-A., McCullagh B., Bilham L., Robben J.,
Langham S.-A., McCullagh B., Bilham L., Robben J.,
Nan der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
Marchert B., Brandt A., Peters S., Van Staveren M., Dirkse W.,
Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
Moijman P., Klein Lankhorst R., Rose M., Hauf J., Ketter P.,
Mooijman P., Klein Lankhorst R., Rose M., Lamberth S., Van den Daele H.,
Nan Montagu M., Rogers J., Cronin A., Quali M., Bray-Allen S.,
Van Montagu W., Rogers J., Cronin A., Quali M., Bray-Allen S.,
A Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
Rettett L., Bloecker H., Scharffe M., Grimm M., Lochnert T.-H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACALARATH STANDARD; PRT; 1069 AA.
0952R1; 0940B3;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potential calcium-transporting ATPase 10, plasma membrane-type
(EC 3.6.3.8) (CA24-ATPASE, isoform 10).
ACALO OR AT4G29900 OR F27B13.140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1; Length 1058;
Pred. No. 8.8e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                        POLY-LEU.
W: CBOE5AB9EDEB9AF2 CRC64;
                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                              EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                          CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
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POLY-GLN.
                                                                                POTENTIAL.
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1058 AA;
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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850
871
890
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DOMAIN
TRANSMEM
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TRANSMEM
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Gabel C., Fuchs M., Maarse A.C., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
Massenet O., Quigley F., Clabald G., Muendlein A., Felber R.,
Chefor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
Chefor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
Chefor F., Wandenbol M., Bargues M., Terol J., Torres A.,
R. Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
Rrishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
Accaria P., Bevan M., Wilson R.K., Mewes H.-W., Stocker S.,
Accaria P., Bevan M., Wilson R.K., Mewes H.-W., Stocker S.,
Accaria P., Bevan M., Wilson R.K., Mewes H.-W., Stocker S.,
Accaria P., Bevan M., Wilson R.K., Ge la Bastide M., Habermann K.,
Askon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
Askon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
Askon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
Antarille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
Antarille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
Antonoiu B., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
Antonoiu B., Zidanic M., Watriansen R., McCombie W., Godhi M., Johnson A.,
Chen E., Marra M., Martienssen R., McCombie W.R.;
Ascurence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NATURE 402:769-777(1999).

-!- FUNCTION: THIS MAGNESTUM DEPENDENT ENZYME CATALYZES THE HYDROLYSIS

OF ATP COUPLED WITH THE TRANSLOCATION OF CALCIUM FROM THE CYTOSOL

INTO THE ENDOPLASMIC RETICULUM (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: ATP + H(2)O + CA(2+)(CIS) = ADP + PHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING DOMAIN, WHICH BINDS CALMODDLIN IN A CALCIUM-DEPENDENT FASHION (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFANTILIS IIB.
CAUTION: THE SEQUENCE CA43665 DIFFERS FROM THAT SHOWN DUE TO WRONG EXON BOUNDARIES PREDICTED FROM THE GENOMIC SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZYME REGGILATION: ACTIVATED BY CALMODULIN (BY SIMILARITY). SUBCELLULAR LOCATION: Integral membrane protein. DOMAIN: THE N-TERMINUS CONTAINS AN AUTOINHIBITORY CALMODULIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Calcium transport; Transmembrane; Phosphorylation;
ATP-binding; Metal-binding; Magnesium; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL161575; CAB79748.1; -.
EMBL; AL050352; CAB43665.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004014; Cation_ATPase.
InterPro; IPR001757; E1-E2_ATPase.
InterPro; IPR001454; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00689; Cation_ATPase_C; 1.
Pfam; PF00690; Cation_ATPase_N; 1.
Pfam; PF00122; E1-E2_ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00119; CATATPASE.
PROSITE; PS00154; ATPASE_E1_E2; 1.
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CYTOPLASMIC (POTENTIAL).

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181 202 2202 220 241 370 330

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DOMAIN TRANSMEM

**LRANSMEM** DOMAIN

POTENTIAL. LUMENAL (POTENTIAL). POTENTIAL.

CYTOPLASMIC (POTENTIAL) LUMENAL (POTENTIAL). POTENTIAL).

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FUNCTION: MEDIATES ATTACHMENT OF STAPHYOCOCCAL CELLS TO
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ilarity 66.7%;
Conservative (
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Best Local Similarity
Matches 4; Conserv
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B3A2_MOUSE
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"Identification and blochemical characterization of the ligand
binding domain of the collagen adhesin from Staphylococcus aureus.";
Biochemistry 32:11428-11435(1993).
                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CXLMODULIN-BINDING (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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MEDLINE-97475225; PubMed-9334749;
Symersky J., Patti J.M., Carson M., House-Pompeo K., Teale M.,
Moore D., Jin L., Schneider A., DeLucas L.J., Hoeoek M.,
                                                                                                                                                                                                                                                                                                                                                                                                                            Lindberg M., Hoeoek M.;
"Molecular characterization and expression of a gene encoding Staphylococcus areus collagen adhesin.";
J. Biol. Chem. 267:4766-4772(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,
                                                                                                                                                                             Score 19; DB 1; Length 1069;
Pred. No. 8.9e+02;
0; Mismatches 2; Indels
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CYTOPLASMIC (POTENTIAL).
                                                                       CYTOPLASMIC (POTENTIAL)
                                   CYTOPLASMIC (POTENTIAL)
                 (POTENTIAL).
                                                     LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                        LUMENAL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                0; Mismatches
                                             POTENTIAL.
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J. Biol. Chem. 269:11672-11672(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-FDA 574;
MEDLINE-92165839; PubMed-1311320;
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                                                                                                                                                                                                                                                                        n 90.5%;
Similarity 66.7%;
4; Conservative
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Best Local Similarity
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EXTRACELLULAR ANCHOR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

COLLAGEN-BINDING.

3 X 187 AA APPROXIMATE TANDEM REPEATS.

LYS/PRO-RICH (CELL WALL-SPANNING).

CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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P13808; O9ES13; O9ES12; O9ES11; Q9ES10; Q9ES09;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Anlon exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SICCAA2 OR AE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-89034212; PubMed-3182834;
Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
"Cloning and characterization of a murine band 3-related cDNA from kidney and from a lymphoid cell line.";
J. Biol. Chem. 263:17092-17099(1988).
COLLAGEN-CONTAINING SUBSTRATA.
SUBGELLULAR LOCATION: TYPE I membrane protein. Cell wall.
SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lecanda J., Urtasun R., Medina J.F.; ^{\prime\prime} Molecular cloning and genomic organization of the mouse AE2 anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY. MEDLINE-20462926; PubMed=11006093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Biochm. Biochms. Res. Commun. 276:117-124(2000).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 1; Length 1183; Pred. No. 9.8e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B6A1CC072E575D76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Cell wall; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB; 1AMX; 24-JUN-98.
InterPro; IPR001899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
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EAGSSS 863
                                                        RESULT 32
MYO6_HUMAN
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                858
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SUBCELLULAR LOCATION: Integral membrane protein.

ALTERNATIVE PRODUCTS: 5 isoforms; a (shown here), bl, b2, c1 and c2; are produced by alternative splicing.

TISSUE SPECIFICITY: Isoform a is widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stomach although they are also detected at lower levels in other tissues. Isoform c1 is stomach-specific. Isoform c2 is expressed at slightly higher levels in lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALMITATE (BY SIMILARITY).
MSSAPRRPASGADSLHT -> MDFLLRPQ (IN ISOFORM
B2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> MPAFQEWKSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00219; ANION EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> G (IN REF. 2).
1A0782C0071782EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IC (POTENTIAL). (ANION EXCHANGE)
                                                                                                                 stomach than in other tissues.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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HIS-RICH.
POLY-SER.
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InterPro: IPR003020; HCO3_cotransp.
Pfam; PP00955, HCO3_cotransp: 1.
PRINWS; PR01231, HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                      EMBL, AF255774; AAC23154.1; -. EMBL, AF255774; AAC23155.1; -. EMBL, AF255774; AAC23156.1; -. EMBL, AF255774; AAC23158.1; -. EMBL, AF255774; AAC23158.1; -.
                                                                                                                                                                                                                                                                            EMBL; J04036; AAA65505.1; -.
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HSSP; P02730; 1BTR.
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1237 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Am. J. Hum. Genet. 69:635-640(2001).

-!- FUNCTION: RECESSIVE ACTIN-BASED MOTOR. REQUIRED FOR STRUCTURAL INTEGRATY OF INNER EAR HAIR CELLS (BY SIMILARITY).

-!- DISEASE: Defects in MYO6 are the cause of an autosomal dominant form of nonsyndromic sensorineural deafness (DFNA22). The deafness is progressive and postlingual, with onset during childhood (8 to 10 years of age at onset of symptoms; 6 to 8 years of age at onset of first audiometric abnormalities). By the age of approximately 50 years, affected individuals invariably have profound sensorineural deafness.
                                                                                                                                                                                                                                                                              Avraham K.B., Hasson T., Sobe T., Balsara B., Testa J.R., Skvorak A.B., Morton C.C., Copeland N.G., Jenkins N.A.;
"Characterization of unconventional MYO6, the human homologue of the qene responsible for deaffness in Snell's waltzer mice.";
Hum. Mol. Genet. 6:1225-1231(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21375673; PubMed=11468689; Melchionda S., Ahiturv N., Biscepila L., Sobe T., Glaser F., Rabionet R., Arbones M.L., Notarangelo A., Di Torio E., Carella M., Zelante L., Estivill X., Avraham K.B., Gasparini P.; "MYG6, the human homologue of the gene responsible for deafness in Snell's waltzer mice, is mutated in autosomal dominant nonsyndromic hearing loss.";
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wells A.L., Lin A.W., Chen L.-Q., Safer D., Cain S.M., Hasson Carragher B.O., Milligan R.A., Sweeney H.L.; "Myosin VI is an actin-based motor that moves backwards."; Nature 401:505-508(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                           Avraham K.B.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
1262 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99447046; PubMed=10519557;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-97402203; PubMed-9259267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head.
Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U90236; AAC51654.2; -. HSSP; P08799; 1LVK.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT DFNA22 TYR-442
                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001609
Pfam; PF00612; IQ;
                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 606346;
MYO6_HUMAN
                                                                                                   Myosin VI.
                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS
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Gaps

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Score 19; DB 1; Length 1237; Pred. No. 1e+03; ); Mismatches 2; Indels

.; 0

4; Conservative

Query Match Best Local Similarity Matches 4; Conserv

90.5%; 66.7%;

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SEQUENCE
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MYO6_MOUSE
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A MEDLINE-20196006; PubMed=10731132;

A Adams M. D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M. D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M. D., Celniker S.E., Holt R.A., Foshurner M., Henderson S.N.,

B George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

B Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazej K.G., Change M., Pfeitfer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej K.G., Change M., Pfeitfer B.D.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M.,

RA Ballew R.M., Basu D.A., Barman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Poster C., Gabriellan A.E., Garg W.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swaroop A., Swaroop M., Garen A.; "Sequence analysis of the complete cDNA and encoded polypeptide for the Glued gene of Drosophila melanogaster."; Proc. Natl. Acad. Sci. U.S.A. 84:6501-6505(1987).
                                                                                                                                                                                                                                                                                                                                                                              DYNA_DROME STANDARD; PRT; 1265 AA.
P13406; Q9VUA1;
01-JAN-1990 (Rel. 13, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
150 kDa dynein-associated polypeptide (DP-150) (Glued
                                                                                                                                                                                                                                                              ó
                                                                                                                                       ATP (POTENTIAL).
ACTIN-BINDING (POTENTIAL).
C -> Y (IN DFNA22).
/FTIG-VAR_012110.
/ WW; CF1FA35796FC1C60 CRC64;
                                                                                                                                                                                                                                   Score 19; DB 1; Length 1262;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                             2; Indels
                                    SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; FALSE_NEG.
MYSSLN; ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil; Disease mutation; Deafness.
                                                                                                                    IQ.
COILED COIL (POTENTIAL).
                                                                                                       MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-OREGON-R, AND CANTON-S;
MEDLINE-87317680; PubMed-2819881;
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                   90.5%;
                                                                                                                                                                                               1262 AA; 146047
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Best Local Similarity 60./~
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665
442
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Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., A Lasko P., Lei Y., Lei Y., Karyen G.H., Ke Z., Kravitz S., Kulp D., Lai Z., Lai X., Lai Y., Lei Y., Lei Y., Lei Y., Lei Y., Lei Y., Lai Y., Murbhy D., Murphy D., Murphy D.M., Nelson D.L., Ra Merkulov G., Mirphy B., Murphy L., Murny D.M., Nelson D.L., Ra Raiazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Rainett K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shug P. S., Randington K., Saunders R.D.C., Scheeler F., Shen H., Shug P. J., Simpson M., Skupski M.P., Smith T., Shug P. J., Laineson M., Skupski M.P., Smith T., Shug Saraman D.A., Weinstock G.M., Weissenbach J., Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Rayers E.W., Rondage T., Worley K.C., Wu D., Yang S., Yao Q. A., Walliams S.M., Woodage T., Worley K.C., Wu D., Zhang G., Zhao Q., Zhao Q., Zhao G., Zh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS THE DYNACTIN 150 KDA SUBUNIT.FAMILY.
-!- SIMILARITY: CONTAINS 1 CAP-GLY DOMAIN.
-!- CAUTION: REF. 1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS AT POSITIONS 32; 174 TO 220; 648 TO 672 AND 1208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FLy...
InterPro: IPRO1302; CAP_GLY: 1.
PROSITE; PSO0845; CAP_GLX_1; 1.
PROSITE; PSS0245; CAP_GLX_2; 1.
Motor protein; Microtubules; Dynein; Coiled coil; Cytoskeleton.

CAP-GLY.

SER-RICH.

SER-RICH.

"OWTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2038A200282B2755 CRC64;
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
D -> A (IN REF. 1).
L -> V (IN REF. 1).
S -> C (IN REF. 1).
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EMBL; AE003536; AAF49788.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A28313; A28313.
FlyBase; FBgn0001108; G1.
InterPro; IPR000938; CAP-Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.5%;
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1084
1160
708
875
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1043
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      888
1043
1265
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1 eagxxs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                         KIAA0232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 36
CUT1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                      AVATABAR K.B., Hasson T., Steel K.P., Kingsley D.M., Russell L.B., Mooseker M.S., Copeland N.G., Jenkins N.A.;

"The mouse Snell's waltzer deafness gene encodes an unconventional myosin required for structural integrity of inner ear hair cells.";

Nat. Genet. 11:369-375(1995).

-!-FUNCTION: RECESSIVE ACTIVE-BASED MOTOR. REQUIRED FOR STRUCTURAL INTEGRITY OF INNER EAR HAIR CELLS (BY SIMILARITY).

-!-TISSUE SPECIFICATY: WIDELY EXPRESSED. WITHIN THE COCHLEA, EXPRESSED SPECIFICALLY WITHIN THE SENSORY HAIR CELLS.

-!-TISSUESECTS IN MYOG ARE THE CAUSE OF SMELL'S WALTTER, A CONDITION CHARACTERIZED BY CIRCLING, HEAD-TOSSING, DEAFNESS AND
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 1; Length 1265; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIN-BINDING (POTENTIAL).
MISSING (IN SNELL'S WALTZER).
W; 4F51ABC72463148C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00015; IQ; 1.
SMART; SM00042; MYSC; 1.
PROSITE; PSS0096; IQ; FALSE NEG.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYOSIN HEAD-LIKE.
                                 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
 PRT; 1265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colled coil; Disease mutation; Deafness, DOMAIN 1 762 MYOSIN HEAL DOMAIN 817 837 IQ.
                                                                                                                                                             MEDLINE=96083582; PubMed=7493015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:104785; Myo6.
InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00063; myosin_head; 4.
                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U49739; AAB00194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.5%;
66.7%;
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 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1265
                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 4; Conserv
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                    HYPERACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
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                                                                                                                                                    IISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 EAGSTS
                      .6-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 eagxxs
MY06_MOUSE
Q64331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y232_HUMAN
                                                                    MYO6 OR SV
                                                         Myosin VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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ID Y232_H
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P53564; 008994; P70301;
01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
CCAAT displacement protein (CDP) (Cut-like 1) (Homeobox protein Cux)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; "Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain."; DNA Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6N;
Wang Z., Goldstein A., Neufeld E.J., Scheuermann R.H., Tucker P.W.;
"Repression of immunoglobulin heavy chain intronic enhancer
through nuclear matrix attachment sites: Cux/CDP homeoprotein is a
component of NF-muNR repressor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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66.7%; Pred. No. 1.1e+03;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. And A. A. Ishikawa K.-I., Ohira M., Kawarabayasi Nagase T., Seki N., Ishikawa K.-Miyajima N., Nomura N.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141663 MW; ZFCFC8837AF8134D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                     Last sequence update)
Last annotation update)
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SEQUENCE OF 64-1395 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                        Hypothetical protein KIAA0232 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97191544; PubMed=9039502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 271-1278 FROM N.A.
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01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
NON_TER 1
SEQUENCE 1278 AA;
                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 EAGSSS 182
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Gaps

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Indels

5;

Mismatches

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Conservative

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Matches
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                                                                                                                                                                                                                                                                                                                                                                 A
BY
                                                                                                                                           SEQUENCE OF 642-1395 FROM N.A.
MEDLINE-96437626; PubMed-8840273;
den Heuvel G.B., Bodmer R., McConnell K.R., Nagami G.T., Igarashi P.;
"Expression of a cut-related homeobox gene in developing and polycystic mouse kidney.";
Kidney Int. 50:453-461(1996).
               MEDLINE-94244481; PubMed-7910552;
Valarche I., Tissier-Seta J.P., Hirsch M.R., Martinez S., Goridis C.,
Brunet J.F.;
                                                               "The mouse homeodomain protein Phox2 regulates Ncam promoter activity in concert with Cux/CDP and is a putative determinant of monnynamitter nhandron".
                                                                                                                                                                                                                                                                                                                             expressed in mouse testis.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY HAS A BROAD ROLE IN MAMMALIAN DEVELOPMENT AS A REPRESSOR OF DEVELOPMENTALLY REGULATED GENE EXPRESSION. MAY ACT B PREVENTING BINDING OF POSITIVELY "ACTIVING CCAAT FACTORS TO PROMOTERS (BY SIMILARITY). COMPONENT OF NE-MUNR REPRESSOR; BINDS TO THE MARS (5' AND 3') OF THE IMMUNOGLOBULIN HEAVY CHAIN
                                                                                                                                                                                                                                                                                              Quaggin S.E., Igarashi P.; {\tt ^A} unique variant of a homeobox gene related to Drosophila cut is
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLUIAR LOCATION: Nuclear.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- SIMILARITY: CONTAINS 3 CUT DOMAINS.
-1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pmental protein; Homeobox; DNA-binding; coil; Alternative splicing.
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G -> A (IN REF. 2).
P -> L (IN REF. 1).
AW; D062CC227D7A163E CRC64;
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STRAIN-A/J, AND BALB/C; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Transcription regulation; Homeobox;
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InterPro; IPR003350; CUT.
InterPro; IPR001356; Homeobox.
Pfam; PF02376; CUT; 3.
Pfam; PF00046; homeobox; 2.
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                                                                                                                                                                                                                                                               SEQUENCE OF 936-1395 FROM N.A.
                                                                                                neurotransmitter phenotype.";
Development 119:881-896(1993)
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EMBL, U46683, AAC52775.1; -.
EMBL; U46684; AAB41146.1; -.
HSSP; P10037; 1AU7.
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1395 AA; 151802
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1079
1178
388
1360
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Coiled coil; A
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DOMAIN
DNA_BIND
DNA_BIND
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CONFLICT
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DOMAIN
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Score 19; DB 1; Length 1395; Pred. No. 1.2e+03;

90.5%;

Query Match Best Local Similarity

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Oshima T., Aiba H., Baba T., Fulita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
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Feng J., Yamanaka K., Niki H., Ogura T., Hiraga S.;
"New killing system controlled by two genes located immediately
upstream of the mass gene in Escherichia coli.";
Mol. Gen. Genet. 243:136-147(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Niki H., Jaffe A., Imamura R., Ogura T., Hiraga S.; "The new gene mukB codes for a 177 kd protein with coiled-coil domains involved in chromosome partitioning of E. coli.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND MUTANTS MUKB33 AND MUKB106 MEDLINE=95080615; Pubmed=7988894;
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                                                                                                                                                                                                                        MUNICAL STANDARD; PRT; 1480 AM. P22523; P77164; 047398; P01-AUG-1991 (Rel. 19, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Cell division protein mukB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMS Microbiol. Lett. 123:27-31(1994).
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STRAIN-K12 / W3110;
MEDLINE-91114703; PubMed-1989883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=562;
                                                            377 EAGSTS 382
1 eagxxs 6
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                                                                                                                                                                                                   MUKB_ECOLI
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Nat. Genet. 1:50-55(1992).
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TRANSFAC; T00100; -.
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Best Local Similarity
                                                                                                                                                       reveals 17 genes.
Genome Res. 8:106
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Q09332;
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DOMAIN
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SEQUENCE
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RWYRYVDSGV (IN REF. 1).
SRRLKGKDISPCRLLFLDEAARLDARSIATLFELCEKLQMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DWMLVLSPRCLNCVSVCKCNSSQRRKISARRKAPPINWCV
KSSRIPNTFWSSACEDLRRNSLKRFQELTKRLLRRVKIKQQ
CRLFFFRKLRFCTKKVAHYGALFFKLLYIRLCKNVRRLYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIIAAPENISPEKGTTYKLVRKVFONTEHVHVVGLRGFAPQ
LPETLPGTDEAPSQAS -> SAACAVKISLLAACCSSMKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
-1- FUNCTION: ESSENTIAL FOR CHROMOSOME PARTITIONING. IMPLICATED IN ATP-DEPENDENT CHROMOSOME PARTITIONING DURING CELL DIVISION.
-1- SIMILARITY: CONTAINS A COILED COIL MYOSIN-LIKE STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Umbilical vein;
MEDLINE-93250973; PubMed=1301999;
Neufeld E.J., Skalnik D.G., Lievens P.M.-J., Orkin S.H.;
"Human CCAAT displacement protein is homologous to the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 1; Length 1486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.2e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKPDE (IN REF. 1).
IM; 38C7874BEB78D6D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUT_HUMAN STANDARD; PRT: 1505 AA. P3980; Q9URV5; 01-FEB-1995 (Rel. 31, Created) 16-OCT-2001 (Rel. 40, Last amnotation update) CCAAT displacement protein (CDP) (Cut-like 1).
                                                                                                                                                                                                                            EMBL; X57550; CAA40776.1; -.
EMBL; D31701; BAA06510.1; -.
EMBL; AE000194; AAC74010.1; -.
EMBL; D90730; BAA35570.1; -.
EMBL; D26440; BAA05459.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1486 AA; 170229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                             PDB; 1QHL; 10-NOV-99.
EcoGene; EG10618; mukB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1134
1175
1277
1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homeoprotein, cut.";
                                                                                                                                                                                                                                                                                                                               PIR; JH0228; JH0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAGATS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 eagxxs 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUTL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
   ACCOCCOS ON REPRESENTATION OF THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
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BY
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                                                            Gloeckner G., Scherer S., Schattevoy R., Boright A., Weber J., Tsul L.-C., Rosenthal A.;
"Large-scale sequencing of two regions in human chromosome 7q22:
analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
                                                                                                                                                                                                                                                                                                                                                                                                          .;
;;
                                                                                                                                                                                                                                         FUNCTION: PROBABLY HAS A BROAD ROLE IN MAMMALIAN DEVELOPMENT AS REPRESSOR OF DEVELOPMENTALLY REGULATED GENE EXPRESSION. MAY ACT PREVENTING BINDING OF POSITIVELY-ACTIVING CCAAT FACTORS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
UDP-glucose:glycoprotein glucosyltransferase precursor (EC 2.4.1.-)
                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear.

ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND ARE PRODUCED BY ALTERNATIVE SPLICING.
DOMAIN: ASN AT POSITION 47 OF THE HOMEOBOX MAY PARTICIPATE IN REGULATING DNA-BINDING ACTIVITY BY PROMOTING HOMO- AND HETERODIMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 3 CUT DOMAINS. SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pfam; pF02376; CUT; 3.

SMART; SM0036; hOmeobox; 1.

PROSITE; PS00027; HOMEOBOX_1; 1.

PROSITE; PS00027; HOMEOBOX_2; 1.

Transcription regulation; HOMEOBOX; Developmental protein; Nuclear protein; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN ISOFORM 2).
W; 860E14D508D4DE11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cing.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUT 1. COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 1; I
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M74099; -; NOT_ANNOTATED_CDS.
EMBL; AF047825; AAC78778.1; -.
                                MEDLINE=99018118; PubMed=9799793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coiled coil; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ψ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003350; CUT.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                   8:1060-1073(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.5%;
SEQUENCE OF 48-224 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164353
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FAMILY
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BINDING
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REPEAT
REPEAT
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                   PATHWAY: GLYCOSYLATION.
SUBUNT: MONOMER.
SUBUNT: MONOMER.
SUBURIT: MONOMER.
SUBURIT: MONOMER.
SUBURIT: MONOMER.

SUBURIT: MONOMER.

SUBURIT: MONOMER.

SUBURIT: MONOMER.

THE EARLIEST EMBRYOS, INCREASING AT 6-8 HRS WITH A MAXIMUM AT 10-12 HRS. IEVELS DECREASE THEREAFTER AND ARE NOT DETECTED IN 18-20 HRS EMBRYOS AND FIRST INSTAR LARVAE BUT IS DETECTED AGAIN AT SECOND INSTAR TO PUPPATION.

SIMILARITY: SOME, TO PREATTON.
                     Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryyota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBL_TaxID=7227;
                                                                                                                                                                                     FUNCTION: UNPOLDED, DENTURED GLYCOPROTEINS ARE SUBSTANTIALLY BETTER SUBSTRATES FOR GLUCOSYLATION BY THIS ENZYME THAN ARE THE CORRESPONDING NATIVE PROTEINS. THIS PROTEIN AND TRANSIENT GLUCOSYLATION MAY BE INVOLVED IN MONITORING AND/OR ASSISTING THE FOLDING AND ASSEMBLY OF NEWLY MADE GLYCOPROTEINS, IN ORDER TO IDENTIFY GLYCOPROTEINS THAT NEED ASSISTANCE IN FOLDING FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                            Parker C.G., Fessler L.I., Nelson R.E., Fessler J.H.,
"Drosophila UDP-glucose:glycoprotein glucosyltransferase: sequence
and characterization of an enzyme that distinguishes between
denatured and native proteins.",
EMBO J. 14:1294-1303(1995).
--- FUNCTION: UNFOLDED. DENATURED GLYCOPROTEINS ARE SUBSTANTIALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
PREVENT SECRETION FROM ER (POTENTIAL)
WW; 95D6849961622DB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Signal; Transferase; Glycosyltransferase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                         COFACTOR: REQUIRES CALCIUM AND MANGANESE IONS FOR ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19; DB 1; Length 1548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UDP-GLUCOSE: GLYCOPROTEIN
(UDP-Glc:glycoprotein glucosyltransferase) (dUGT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUCOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2035 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 23-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                    MEDLINE-95246722; PubMed-7729408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HMP2_YEREN STANDARD; FP48633; Ol-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U20554; AAA85850.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1545 1548
1548 AA; 174465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0014075; Ugt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                RFAI PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
266
864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 EAGSTS 260
                                                                                                                                                                                                                                                               CHAPERONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 eagxxs 6
                                                                                                       TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HMP2_YEREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- DOMAIN: CONSISTS OF A CENTRAL REGION WITH SIMILARITY TO THE REPEAT DOMAINS OF ACVS AND GRC2, FIANKED BY TWO REPEAT DOMAINS, EACH OF WHICH CONTAINS 5 DIRECT REPEATS.
-i- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                              "High-molecular-weight protein 2 of Yersinia enterocolitica is homologous to AngR of Vibrio anguillarum and belongs to a family of proteins involved in nontibosomal peptide synthesis.";

J. Bacteriol. 175:5488-5504(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
PHOSPHOPANTETHEINE (BY SIMILARITY).
                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                     Guilvout I., Mercereau-Puijalon O., Bonnefoy S., Pugsley A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF SMALL PEPTIDES.
-!- COFACTOR: CONTAINS 3 COVALENTLY BOUND PHOSPHOPANTETHEINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ligase; Multifunctional enzyme; Phosphopantetheine; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1C801377A4375BDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11- SIMILARITY: CONTAINS 3 ACYL CARRIER DOMAINS.
01-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) High-molecular-weight protein 2 (HMWP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L18881; AAA27636.1; --
EMBL; 235454; CAA84606.1; --
BSP; A48654, A48654.

InterPro; IPR000873; AMP-bind.

InterPro; IPR001242; DUF4.

InterPro; IPR001242; DUF4.

InterPro; IPR001051; SAM_bind.

InterPro; IPR001051; SAM_bind.

Pfam; PF005501; AMP-binding; 1.

Pfam; PF00550; Pp-binding; 3.

PRINTS; PR00550; AMPBINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS00455; AMP_BINDING; 1.
PROSITE; PS50075; ACP_DOMAIN; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          II-DR2.
II-DR3.
II-DR4.
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                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93374844; PubMed=8366034;
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                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-8081 / SEROTYPE 0:8;
                                                                                                                                  Versinia enterocolitica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1475 2014
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1849
                                                                                                                                                                                                                        NCBI_TaxID=630;
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Length 2035;

DB 1;

90.5%; Score 19;

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Query Match
Best Local Similarity
Matches 4; Conserv
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O14904;
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SEQUENCE
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Capsella.
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                MEDLINE-99274088; PubMed-10344291; Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C.; Prigerio J.-M. Plomion C.; Reparation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBL_TaxID=71647;
                                                                                                                                                                                                                                                                                                                                                                                                                     THIS PROTEIN
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                       ő
                                                                                                                                                                                                                                                                                                                                              proteins.";
Electrophoresis 20:1098-1108(1999).
-1- FUNCTION: MAY INTERACT WITH A CLPP-LIKE PROTEASE INVOLVED
DECRADATION OF DENATURED PROTEINS IN THE CHLOROPLAST (BY
                                                                                                                                                                 15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ATP-dependent clp protease ATP-binding subunit clpA homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).

-!- SUBCELLULANE LOCATION: Chloroplast (By similarity).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF (SPOT N9) IS: 5.9, ITS MW IS: 92 kDa.
-!- SIMILARITY: BELOWS: TO THE CLPA/CLPB FAMILY.
-!- PROSITE; PSO0870; CLP_AB.
--- PROSITE; PSO0870; CLPAB_I; PARTIAL.
--- PROSITE; PSO0871; CLPAB_I; PARTIAL.
--- PROSITE; PSO0871; CLPAB_I; PARTIAL.
--- Chaperone; ATP-binding; Repeat; Chloroplast.
--- ATP-binding; Repeat; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE.
Scawen M.D., Ramshaw J.A.M., Brown R.H., Boulter D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44B5950B73A96152 CRC64;
Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 1;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                30 AA.
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                                                                                                                                                                                                                Pinus pinaster (Maritime pine)
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66.78;
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         66.78;
                       Conservative
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                                                                                                                                STANDARD;
           Best Local Similarity Matches 4; Conserv
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Matches 4; Conserv
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                                                                     1972 EAGATS 1977
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15-JUL-1999
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NON_TER
SEQUENCE
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                                                                                                         RESULT 41
CLPA_PINPS
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PLAS_CAPBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                        Baltimore (1977).
-!- FUNCTION: PLASTOCYANIN PARTICIPATES IN ELECTRON TRANSFER BETWEEN P700 AND THE CYTOCHROME B/F COMPLEX IN PHOTOSYSTEM I.
-!- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE
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Unpublished results, cited by:
Souther D., Haslett B.G., Peacock D., Ramshaw J.A.M., Scawen M.D.;
(In) Northcote D.H. (eds.);
Plant biochemistry II, pp.13:1-40, University Park Press,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WNTI5) is closely linked to WNT3 on human chromosome 17q21."; Genomics 46:450-458(1997).
-1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY.OF SEVEN TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY SIGNALING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bergstein I., Eisenberg L.M., Bhalerao J., Jenkins N.A.,
Copeland N.G., Osborne M.P., Bowcock A.M., Brown A.M.C.;
"Isolation of two novel WNT genes, WNT14 and WNT15, one of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Copper; Thylakoid; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASTOCYANIN-LIKE.

COPPER (BY SIMILARITY).

30BA97B58B9580F1 CRC64;
                                                                                                                                                                  MEMBRANE SURFACE IN CHLOROPLASTS.
-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
PIR; A00304; CUSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 1; Len
Pred. No. 1.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AA
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                                                                                                                                                                                                                                                    HSSP, P00289; 2PCF.
Mendel; 11575; CAPbu; PetE;1.
InterPro; IPR001235; Copper_blue.
InterPro; IPR001235; Copper_blue.
Pfam; PF00127; copper_blue1.
PRINTS; PR00156; COPPERBUDE.
ProDom; PD001235; Copper_blue; 1.
PROSITE; PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Cop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10383 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNT-14 protein (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
87
92
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
                or send an email to license@isb-sib.ch)
                                       EMBL; L09228; AAA67475.1; -.
EMBL; X73898; CAA52103.1; -.
EMBL; Z99116; CAB14268.1; -.
PIR; S45537; S45537.
HSSP; Q77450; 1A58.
Subtilist; BG10512; ppiB.
InterPro; IPR002130; CSA_PPIASE.
PRAMYS; PR00105; CSA_PPIASE.
PROSITE; PS00170; CSA_PPIASE.
PROSITE; PS00772; CSA_PPIASE_1; 1.
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MEDLINE-86258168; PubMed-2425311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%;
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 85.7
Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 EAGTVS 138
                                                                                                                                                                                                                                                                                                                                                  82 EAGALS 87
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                                                                                                                                                                                                                                                                                                                     1 eagxxs 6
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Q28183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herrler M., Bang H., Marahiel M.A.; "Cloning and characterization of ppiB, a Bacillus subtilis gene which encodes a cyclosporin A-sensitive peptidyl-prolyl cis-trans isomerase.";
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-168 / MARBURG;
MEDLINE-95020538; PubMed-7934829;
STOKIN A.V., ZUMSTEAL E., Azevedo V., Ehrlich S.D., Serror P.;
Strokin A.V., zumstein E., Azevedo V., Ehrlich S.D., Serror P.;
"The organization of the Bacillus subtilis 168 chromosome region between the spovA and serA genetic loci, based on sequence data.";
Mol. Microbiol. 10:385-395(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168 / JH642;

MEDLINE-96445629; PubMed-8755892;

Graumann P., Schroeder K., Schnid R., Marahiel M.A.;

"Cold shock stress-induced proteins in Bacillus subtilis.";

"Cold shock stress-induced proteins in Bacillus subtilis.";

"Bacteriol. 178:4611-4619(1996).

-I- FUNCTION: PPIASES ACCELERATE THOEDING OF PROTEINS.

-I- CAPALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOREPTIDES.

-I- ENZYME REGULATION: INHIBITED BY CYCLOSPORIN A (CSA).

-I- SUBCELLULAR LOCATION: CYCOPLASMIC (By similarity).

-I- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Peptidyl prolyl cis-trans isomerase B (EC 5.2.1.8) (PPIase B)
                                                                                                                                                                                                     Score 18; DB 1; Length 123; Pred. No. 2e+02;
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                                                                                                                                                         123 AA; 13143 MW; 8F000D2568EEA744 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                143 AA.
                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SUBJUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-168 / JH642;
MEDLINE-94293776; Pubmed-8022278;
 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus/Staphylococcus group; Bacillus NCBI_TaxID=1423;
                                             InterPro; IPR000970; Wntl.
Pfam; PF00110; wnt; 1.
SMART; SM00097; WNTl; 1.
PROSTTE; PS00246; WNTl; 1.
Developmental protein; Glycoprotein.
NON_TER 123 123
SEQUENCE 123 AA; 13143 MW; BF000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Microbiol. 11:1073-1083(1994).
                           EMBL; AF028702; AAC39550.1; -.
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66.7%;
                                                                                                                                                                                                                                 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-26
                                                                                                                                                                                                                                                                                       43 EAGAIS 48
                                          602863; -
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P35137:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakagawa Y., Kuo C.H., Ishli K., Shiosaka S., Tohyama M., Miki N.; "Cloning and characterization of a cDNA specific for bovine retina."; Neurosci. Res. 3:300-310(1986).
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olimov-1997 (Rel. 35, Created)
Ol-NOV-1997 (Rel. 35, Last sequence update)
Ol-NOV-1997 (Rel. 35, Last annotation update)
Retina-specific 15.7 kDa protein.
Bos taurus (Bovine).
Bos taurus (Actional Protein (Bovine).
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                               ő
                                                                                                                                     Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
Isomerase; Rotamase; Complete proteome.
SEQUENCE 143 AA; 15256 MW; 9EF17D70EB81EC51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M34915; AAA30756.1; -.
SEQUENCE 147 AA; 15658 MW; 1FEDA48788B39645 CRC64;
                                                                                                                              85.7%; Score 18; DB 1; Le
66.7%; Pred. No. 2.3e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 1; 1
Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AA.
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bask-853-claim4.rsp

155 AA.

PRT;

STANDARD;

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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
Molybdopterin converting factor subunit 2 (MPT synthase subunit 2)
Molybdopterin synthase subunit 2) (Molybdopterin synthase subunit 2)
Molybdopterin synthase subunit 2)
Molybdopterin synthase subunit 2)
Molybdopterin Synthase subunit 2)
MOAE OR R01168 OR SWC00599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21396507; PubMed=11481430; Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godier T., Goffeua A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; Analysis of the chromosome sequence of the legume symbiont
                                                                                                                                                                                                                                                                                                                                  Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=382;
                           RESULT 47
MOAE_RHIME
ID MOAE_RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P58233;
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CEST_ECO57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DoBby R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Δ.
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S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains..;
submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THIS ENZYME IS INVOLVED IN NUCLEOTIDE METABOLISM: IT PRODUCES DUMP, THE INTRACELLULAR CONCENTRATION OF DUTP SO THAT URACIL CANNOT BE INCORPORATED INTO DNA (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: dTTP + H(2)0 = dUMP + diphosphate...
-!- PATHWAY: DE NOVO SYNTHESIS OF THYMIDYLATE...
-!- SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
                                                                                                                                                                                                                                                             Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=9892987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd 'Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeper K., Skelton S., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Pociphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%; Score 18; DB 1; Length 154; 66.7%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 10; Pred. No. 2.5e+02; Pred. No. 2.5e+02; Indels
                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probom; PD000946; duTPase; 1.
Hydrolase; Nucleotide metabolism; Complete proteome.
SEQUENCE 154 AA; 15803 MW; 836D5E6420EF455B CRC64;
                                                                                                                                    (durpase) (durp pyrophosphatase).
Dur or RV2697C OR MT2771 OR MTCY05A6.18C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interPro; IPR001428; dUTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE007106; AAK47086.1;
HSSP; P06968; 1EUW.
                                                                                                                                                                                                 Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00692; dUTPase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 296072; CAB09487.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuberculist; Rv2697c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
-!-FUNCTION: Converts molybdopterin precursor Z into molybdopterin.
This requires the incorporation of two sulfur atoms into precursor Z to generate ae dithiolene group (By similarity).
-!- PATHWAY: Molybdenum cofactor biosynthesis.
-!- SUBUNIT: Heterodimer of 2 moaD subunits and 2 moaE subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.7%; Score 18; DB 1; Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; 2.5e+02;
Pred. No. 2.5e+02;
Pred. Tarthes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOIYbdenum cofactor blosynthesis; Complete proteome.
SEQUENCE 155 AA; 16926 MW; 4DE035E7ADFBB367 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 AA
                                                                                                                                                                                        similarity).
-!- SIMILARITY: BELONGS TO THE MOAE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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CEST OR 25111 OR ECS4560 OR L0026.
Escherichia coli 0157.H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL591786; CAC45747.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003448; MoaE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02391; MoeA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 EAGALS 48
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                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-0157:H7 / KIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi W., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shihada T., Ahttori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli Comparison with a laboratory strain K-12.";
                                                                                                                 SEQUENCE FROM N.A.
STRAIN-LDS:147 / EDL933 / ATCC 700927;
STRAIN-LOS:147 / EDL933 / ATCC 700927;
MEDLINE-98339885; PubMed-9673266;
Perna N.T., Mayhew G.F., Posfai G., Elliott S., Donnenberg M.S.,
Raper J.B., Blattner F.R.;
"Molecular evolution of a pathogenicity island from enterohemorrhagic
Escherichia coli 0.157:147."
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=96079490; PubMed=8566710;
Zhao S., Mitchell S.E., Meng J., Doyle M.P., Kresovich S.;
"Cloning and nucleotide sequence of a gene upstream of the eaeA gene of enterohemorrhagic Escherichia coli 0157:H7.";
FEMS Microbiol. Lett. 133:35-39(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21074935, PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.7%; Score 18; DB 1; Length 156; 66.7%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 AA; 17681 MW; 999545426E26D2D6 CRC64;
                                                                                                                                                                                                            Infect. Immun. 66:3810-3817(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32312; AAB00110.1; -.
EMBL; AF071034; AAC31505.1; -.
EMBL; AE005595; AAG58824.1; -.
EMBL; AP002566; BAB37983.1; -.
Chaperone; Virulence.
SEQUENCE 156 AA; 17681 MW; 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 eagxxs 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson D.A., Ramphal R., Lory S.;
"Characterization of Pseudomonas aeruginosa filo, a gene involved in flagellar biosynthesis and adherence.";
Infect. Immun. 63:2950-2957(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-2043733; PubMed=10984043; Strain-ATCC 15692 / PAO1; MEDLINE-20437337; PubMed=10984043; Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hinfnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
--- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
--- SIMILARITY: BELONGS TO THE FLIN/MOPA/SPAO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.7%; Score 18; DB 1; Length 157;
66.7%; Pred. No. 2.5e+02;
live 0; Mismatches 2; Indels
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ProDom; PD001777; SpoA; 1.
Chemotaxis; Flagella; Flagellar rotation; Inner membrane;
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B3D91C0182ACB775 CRC64;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                           Flagellar motor switch protein flin.
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95347807; PubMed=7622217;
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Nature 406:959-964(2000).
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Matches 4; Conservative
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                                                                                                                                                             Pseudomonas aeruginosa
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RESULT 50

RESULT 49 FLIN\_PSEAE

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedisb-sib.ch).
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                                                                                                                                                                                                                                                                                           Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Faveln A.,
Fulton L., Gardner A., Greshaw J., Kirsten J., Lalister L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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Pred. No. 2.6e+02;
0; Mismatches 2; Indels
                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 17.2 kDa protein F58A4.2 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; $40974; $40974;
Wormbep; F5884.2; CE01017.
Hypotherical protein.
SEQUENCE 159 AA; 17201 MW; 364FE35A65E2C89D CRC64;
159 AA.
PRT;
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MEDLINE-94150718; PubMed-7906398;
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Best Local Similarity 66.7
Matches 4; Conservative
STANDARD;
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                                                                                                                                     Caenorhabditis elegans.
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Search completed: August 30, 2002, 15:11:55 Job time: 311 sec

145 EAGSGS 150

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Q92d00 listeria in Q92d00 listeria in Q91306 rana catesb Q9hstl halobacteri Q91307 rana catesb Q9xf64 arabidopsis Q912f6 arabidopsis Q92r3 staphylococ Q92hn7 filzoblum mos Q92hn7 filzoblum mos Q94hff volvio chol Q9v64 drosophila Q9ait5 vibrio chol Q9363 arabidopsis Q9f65 araa catesb Q91266 rana catesb Q91266 rana catesb Q91266 rana catesb Q91266 rana catesb Q9pcj6 xylella fas Q90370 coturnix co Q9pua6 xenopus lae Q9543 homo sapien Q9hffi homo sapien
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O98183 brachydanio
O98186 arundinella
O9818 rhizobium 1
09842 rhizobium m
098085 brachydanio
073679 brachydanio
023101 arabidopsis
099191 caenorhabdi
099191 rattus norv
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF281817; AAK57118.1; -
SEQUENCE 108 AA; 11188 MW; 5732B2C61DBDE820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA stage; Herpesviridae;
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Last annotation update)
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Pred. No. 5.8e+02;
0; Mismatches 2;
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                                                 Q9HST1
Q91ST6
Q91ZJ6
Q91ZJ6
Q91SN7
Q92NN7
Q98196
Q9DCE4
Q9ATT5
Q91ZF6
Q91ZF6
Q91ZF6
Q91ZF6
Q91ZF6
Q9DCF6
Q9
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O73679
O23101
Q9BL91
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Q9ATS6
Q981H9
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J. Virol. 75:4854-4870(2001).
[2]
SEQUENCE FROM N.A.
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illarity 66.7%;
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tupaia herpesvirus.
Viruses; dsDNA viruses,
Betaherpesvirinae.
NCBI_TaxID=10397;
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Best Local Similarity
Matchés 4; Conserv
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1 eagxxs
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 Q91TM3
Q91TM3;
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 291TM3
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Q9ybx6 aeropyrum p
Q9kru8 vibrio chol
Q9kri5 oryza sativ
Q9awi9 oryza sativ
Q9xwi5 arabidopsis
Q9bs09 homo sapien
G9wil homo sapien
G9wil homo sapien
G9mzll oryctolagus
Q9mzll oryctolagus
Q9113 oryza sativ
Q1114 caenorhabdi
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Q9hpe3 halobacteri
O36890 human immun
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25.139 Million cell updates/sec
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                                                                                                              August 30, 2002, 15:05:49; Search time 41.29 Seconds
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 50 summaries
                                                                                 OM protein - protein search, using sw model
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Q9XIK5
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Q9KRU8
Q9FRJ5
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Gapop 10.0 , Gapext 0.5
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Q36890
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Q9MZ11
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sp_phage:*
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sp_unclassified:*
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sp_bacteria:*
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sp_rodent:*
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Maximum DB
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130 AA; 14476 MW; 9053DD2EF3A3E00F CRC64;
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MEDLINE=99310339; Pubmed=10382966;
                                   90.5%;
66.7%;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                          Conservative
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Matches 4; Conserv
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NCBI_TaxID=56636;
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 SEQUENCE
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RA SEQUENCE FROM N.A.

RA MEDLINE-2050483; PubMed=11016950;

RA MEDLINE-20504483; PubMed=11016950;

RA SHARIZEH S.V. Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

RA SWATZEL S.V. Weiler N., Hall J., Dahl T.A., Welti R., Goo Y.A.,

RA Alam Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

RA Alam M. Frelias T. Hou S.V. Danis P.P., Omer A.D.,

RA Alam M. Frelias T. Hou S.V. Danis P.P., Omer A.D.,

RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

RT "Genome sequence of Halobacterium species NRC-1.";

RT "Genome Sequence of Nacional S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-97445059; Pubmed-9300048;

Leigh Brown A.J., Lobidel D., Wade C.M., Rebus S., Phillips N.,

Brettle R.P., France A.J., Leen C.S., McMenamin J., McMillan A.,

Maw R.D., Mulcahy F., Robertson J.R., Sankar K.N., Scott G., Wyld R.,

Peutherer J.E.;

"The molecular epidemiology of human immunodeficiency virus type 1 in

six cities in Britain and Ireland.";

Virology 235:166-177(1997).

EMBL, AF014287; AACS8368.1;

InterPro; IPR000071; Retroviral_gag_pl7.

Pfam; PP00540; gag_pl7; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.5%; Score 19; DB 17; Length 122; Best Local Similarity 66.7%; Pred. No. 6.6e+02; Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                       Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriaceae;
                                                                                           01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01.JAN-1998 (TrEMBLrel. 05, Created)
01.JAN-1998 (TrEMBLrel. 05, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
GAG POLYPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                      122 AA
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NON_TER 1 1
NON_TER 130 130
                                                                      PRELIMINARY;
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 111 | 30 EAGASS 35
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Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hombach-Klonisch S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klonisch T., Froehlich C., Tetens F., Fischer B., Hombach-Klonisch S.; "Molecular remodeling of members of the relaxin family during primate
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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   Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evolution.";
Mol. Biol. Evol. 0:0-0(2001).
I. SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
I. SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
I. STHAILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF317624; AG642317.1;
EnterPro: PRO0078; InSulin_IGF_relaxin.
SMART; SMO0078; InSulin_IGF_relaxin.
PROSITE; PSO0262; INSULIN; 1.
SEQUENCE 131 AA; 14414 MW; FIBAFA9ACFC85943 CRC64;
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Score 19; DB 15; Length 13
Pred. No. 7.1e+02;
0; Mismatches 2; Indels
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Last annotation update)
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NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TEMBLrel. 16, Last annotation update)
HYPOTHETICAL 15.7 KDA PROTEIN APE1474.
                                                                                                                                                                                                                                                                                                                                                                                                                131 AA.
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Length 149; Indels

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Shinn P., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Kim C., Walker M., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S.,
               Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J., Zismann V., Pai G., Bowman C.L., Frijii C.Y., VanAken S.E., Bowman C.L., Craven B., Utterback Y.R., Khalak H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; "Oryza sativa chromosome 10 BAC OSJNBb0064P21 genomic sequence."; Submitted ANG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AC073166; AAG46108.1; -. Hypothetical protein.

SEQUENCE 149 AA; 15284 MW; 8B71E9231087266 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0489A05.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003105; BAB32988.1; -
SEQUENCE 151 AA; 16103 MW; 6E942A203BC62C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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ches 2;
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Pred. No. 8.1e+02;
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; Mismatches
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66.7%; Pred. No.
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STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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(TrEMBLrel. 17, I
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Best Local Similarity 66.7%;
Matches 4; Conservative
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12,
19,
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01-JUN-2001 (TrEMBLrel.
P0489A05.8 PROTEIN.
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01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
 NIPPONBARE;
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                  111 EAGASS 116
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 STRAIN-CV.
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MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tertelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                               Gaps
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
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                                                                                                                           Length 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
             DNA Res. 6:83-101(1999).
EMBL, AP000061; BAR80472.1; -
HYPOTHETICAL protein; Complete proteome.
SEQUENCE 143 AA; 15708 WW; C40E29CBB0AF6892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
SEQUENCE 145 AA: 15726 MW; 976EIF5EB50DB0EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9FRJ5;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 15.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                              01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN VC1536.
                                                                                                                       Score 19; DB 17; I
Pred. No. 7.8e+02;
0; Mismatches 2;
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crenarchaeon, Aeropyrum pernix Kl.";
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                                                                                                                       90.5%;
ilarity 66.7%;
Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholerae.
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Streptomyces glaucescens.

Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBL_TaxID=1907;
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
5-FT1A (FRAGMENT).
Cryctolagus cuniculus (Rabbit).
Gryctolagus cuniculus (Rabbit).
Mammalia: Butheria: Chordata: Craniata: Vertebrata; Euteleostomi; Mammalia: Eutheria: Lagomorpha; Leporidae; Oryctolagus.
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STRAING-LA.0;
MEDLINE=95352622; PubMed=7626609;
Summers R.G., Ali A., Shen B., Wessel W.A., Hutchinson C.R.;
Summers R.G., Ali A., Shen B., Wessel W.A., Hutchinson C.R.;
Malonyl-coenzyme A:acyl carrier protein acyltransferase of
Streptomyces glaucescens: a possible link between fatty acid and
polyketide biosynthesis.";
Biochemistry 34:9389-9402(1995).
EMBL: L43074; AAA99450.1; -.
SEQUENCE 164 AA: 18203 MW; CBOECF031044BB09 CRC64;
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TISSUB-RETINA;
POOCDANARIL K., HUNTER D.D., Brunken W.J.;
PootDanakit K., Hunter D.D., Brunken W.J.;
"5-HTA and 5-HT7 Receptor Expression in the Mammalian Retina.";
Brain Res. 0:0-012000);
EMBL; APZ569231; AAF76184.1; -.
INTERFO: IPR000276; GPCR_Rhodpsn.
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      Length 161;
                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FABD, FABH, FABC, FABB, AND ORF5 GENES.
Score 19; DB 4; I
Pred. No. 8.8e+02;
0; Mismatches 2;
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   Query Match
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Q54209;
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Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.; "Genomic sequence for Arabidopsis thaliana BAC T10024 from Chromosome
                                                                                                                                                                                                                                                                                                                              Gaps
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 17.1 KDA PROTEIN.
HYPOTHETICAL 17.1 KDA PROTEIN.
HYPOTHETICAL 17.1 KDA PROTEIN.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation update)
CDNA FLJ20847 FIS, CLONE ADKA01746.
Homo sapiens (Human).
Bukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
Hirao M., Ohmoril Y., Ota T., Suzuki Y., Obayashi M., Nishi T.,
Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FRB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO00854; EAA1939.1;
SEQUENCE 161 AA; 17118 MW; 11098ABIEA15D7IC CRC64;
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Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005805. AAH05805.1; -.
Hypothetical protein.
SEQUENCE 161 AA; 17058 MW; E4098ABIF0A5D706 CRC64;
                                                                                                            Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC007067; AAD39566.1; -. SEQUENCE 152 AA; 17676 MW; A7053F4DA73C3490 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 AA.
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          138 EAGTTS 143
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Q9NW11
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U61958; ABR03180.1; -.
Hypothetical protein.
SEQUENCE 200 AA; 22012 WW; 66A23EDA709C66B2 CRC64;
                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
  'Direct Submission.";
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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STRAIN-CV. NIPPONBARE;
Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                       094LT3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 19.8 KDA PROTEIN.
OVYZA sativa (Rice).
Eckaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                      "Oryza sativa chromosome 10 BAC OSJNBb0011A08 genomic sequence.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC034258; AAK54288.1; -.
Hypothetical protein.
SEQUENCE 192 AA; 19819 MW; 4CE8C88AE83DF374 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 10; Length 192;
Pred. No. 1.1e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The sequence of C. elegans cosmid C25A8.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
                                                                               192 AA.
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MEDLINE-99069613; PubMed-9851916;
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01-NOV-1996 (TrEMBLrel. 01, La
01-DEC-2001 (TrEMBLrel. 19, La
HYPOTHETICAL 22.0 KDA PROTEIN.
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Latreille P., Stellyes L.;
"The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.5
Best Local Similarity 66.7
Matches 4; Conservative
                                                                               PRELIMINARY;
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STRAIN-BRISTOL N2;
Waterston R.;
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                                                                                                                                                                                                 NCBI_TaxID=4530;
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                    142 EAGAAS 147
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1 eagxxs 6
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglumeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcook K., Basham D., Brown D., Chillingworth T., Connor R.,
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Bacteria, Firmloutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
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Score 19; DB 5; Length 200; Pred. No. 1.1e+03; ); Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
Scalence 282:2012-2018 (1998).
Extence 282:2015; CABOL136.1; -
SEQUENCE 201 AA; 22266 MW; EC0423A8D7DDE4FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JDC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETCAL 21.6 KDA PROTEIN.
MOAE3 OR RV3322C OR MTV016.22C.
                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.1e+03;
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MEDLINE=99069613; Pubmed=9851916;
90.5%;
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                                                 Conservative
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Matches

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RESULT 18

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MEDLINE-20504483; PubMed=11016950; Merquist B., Pan M., MEDLINE-20504483; PubMed=11016950; May W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swarzzell S., Welt D., Hall T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Genome sequence of Halobacterium species NRC-1.; Passarma S.; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                         Solc C.F., Derfler B.H., Duyk G.M., Corey D.P.;
"Molecular cloning of myosins from the bullfrog saccular macula: A candidate for the hair-cell adaptation motor.";
Aud. Neurosci. 1:63-75(1994).
EMBL: U14380; AAA5089.1; -.
HSSP; P08799; 1MND.
                                                                                                  Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 231;
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Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 13; Length 23
Pred. No. 1.3e+03;
0; Mismatches 2; Indels
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SEQUENCE 245 AA; 26216 MW; A26FBBBCFAA5DB78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25693 MW; D3FFF5C343E6FAC8 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
L-ISOASMATYL PROTEIN CARBOXYL METHYLTRANSFERASE.
PIMTI OR VNGO089G.
                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 AA.
              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00063; myosin_head. Probom; PD000355; myosin_head; 1. NoN_TER 1
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        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, MYOSIN VI (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.5%;
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Best Local Similarity
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SEQUENCE 231 AA;
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                    TISSUE-SACCULE;
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              ACCOCCOS SELECTION OF SELECTION
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Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Selston J.E., Taylor K., Whitehead S., Barrell B.G.; Parlor J.E., Taylor K., Whitehead S., Barrell B.G.; Nature 393:537-544(1998).

Nature 393:537-544(1998).

FMBL, ALO21841, CAA17094.1; -.

Tuberculist, Rv3322c; -.

InterPro; IPR000051; SAM_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1.2e+03;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 204 AA; 21614 MW; 13C5CB74C9C4B07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23672 MW; CB73DB2965A08F99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 16;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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STRAIN-CLIP 11262 / SEROVAR 6A;
PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 294:849-852(2001).
EMBL; AL596167; CAC96252.1; -.
ListiList; LIN01021; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 EAGTAS 158
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Bloecker H., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress). Eukaryophyta; Tracheophyta; Eusaryots; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
Pred. No. 1.4e+03;
                                                                                                                                                                                   257 AA.
                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                   PRT;
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milarity 66.7%;
Conservative (
                 66.78;
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01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                 Conservative
                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
Matches 4; Conserv
               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                              184 EAGSSS 189
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                                                                                                                                                                                   09LZJ6
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                             Matches
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MEDLINE=99408259; PubMed=10480382;
Salinas-Mondragon R.E., Garciduenas-Pina C., Guzman P.;
"Early elicitor induction in members of a novel multigene family coding for highly related RING-H2 proteins in Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                        Rana catesbelana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                  Solc C.F.; Derfler B.H., Duyk G.M., Corey D.P.;
"Molecular cloning of myosins from the bullfrog saccular macula:
candidate for the hair-cell adaptation motor.";
Aud. Neurosci. 1:63-75(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 13; Length 25
Pred. No. 1.4e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB8395E86BD6DE93 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RING-H2 ZINC FINGER PROTEIN ATL5.
                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Mol. Biol. 40:579-590(1999).
-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AF132015; AAD33583.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                 254 AA.
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                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00063; myosin_head; 3.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254
29039 MW;
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Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28608 MW;
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                                                                                                                                             01-NOV-1996 (TrEMBLEEL. 01,
01-NOV-1996 (TrEMBLEEL. 01,
01-DEC-2001 (TrEMBLEEL. 19,
MYOSIN VI (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U14381; AAA65090.1;
HSSP; P10587; 1BR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                               PRELIMINARY;
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Best Local Similarity
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|151 EAGAAS 156
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Zinc-finger
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Matches

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**Q9XF64** RESULT 22

**09XF64** 

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                                                                                                                                                                                                                                     Length 257;
                                                                                                                                                                                                                                                                               Indels
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; ALI65651; CABB3119.1; -.
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HG4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                       257 AA; 28592 MW; B6B7595DFF528431 CRC64;
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Last annotation update)
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Bacteria: Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_FaxID=158879;
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Pred. No. 1.4e+03;
); Mismatches 2;
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Gaps

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Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M., Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D., Kahn M.L., Kaling D.H., Kiss E., Komp C., Lelaure V., Masuy D., Palman S., Keating D.H., Kiss E., Komp C., Lelaure V., Ramsperger U., Surzycki R., Thebault P., Vandenbol M., Porhoelter F.J., Weils D.H., Wong K., Yeh K.-C., Batut J.; The composite genome of the legume symbiont Sinorhizobium meliloti."; Science 293:668-672(2001).

EMBL, AL591790, CAC46806.1; -. Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chu R., Leng X., Bao Y., Pu 2., Pan N., Chen 2.; "Amplification of soybean mosaic virus coat protein gene by polymerase chain reaction and its sequence analysis."; Acta Bot. Sin. 34:523-528(1992).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
COAT PROTAIN (FRABMENT).
Soybean mosain (FRABMENT).
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Soybean mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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                                                                                                                                                                          90.5%; Score 19; DB 16; Length 26.66.7%; Pred. No. 1.4e+03;
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Pred. No. 1.5e+03;
0; Mismatches 2; Indels
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InterPro: IPR001592; POty_coat. Pfam; PF00767; Poty_coat.; L. SEQUENCE 266 AA; 30084 MW; 4E08AFE7D434307F CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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NCBI_TaxID=12222;
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NCBI_TaxID=12222;
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Q88190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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MeDLINE-98340502; PubMed=9675851;
Neubauer H., Pantel I., Gotz F.;
Neubauer H., Pantel I., Gotz F.;
Neubauer H., Pantel I., Gotz F.;
Note to the molybdenum cofactor biosynthesis gene cluster in Staphylococcus carnosus.";
FEMS Microbiol. Lett. 164:55-62(1998).
EMBL; AF109295; AAC83133.1;
EMBL; P37329; UMOD.
SEOUENCE 261 AA; 29203 MW; 126A2D314BBAFB13 CRC64;
                                                                                                                       Length 260;
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Pred. No. 1.4e+03;
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Pred. No. 1.4e+03;
0; Mismatches 2; Indels
                                                                            29117 MW; 7A5D4A01A4482C4D CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus carnosus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
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                    Lancet 357:1225-1240(2001).
EMBL; AP003136; BAB43371.1; -.
HSSP; P37329; 1WOD.
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66.7%;
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Best Local Similarity 66.7%;
Matches 4; Conservative (
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Best Local Similarity
Matches 4; Conserv
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                                                               Complete proteome
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Medine-2108560; PubMed-11217851;

Medine-2108560; Medine-210858;

Medine-2108560; Medine-21088;

Medine-2108560; Medine-21088;

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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
NCBI_TaxID=10090;
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Pred. No. 1.5e+03;
0; Mismatches 2; Indels
                                                               CDNA sequence of the gene encoding coat protein of SMV.";
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SEQUENCE 269 AA: 31242 MW; B549CB553DEB6568 CRC64;
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                                                                            Nucleic Acids Res. 0:0-0(0).
EMBL; X63771; CAA45307.1; -.
InterPro; IPR001592; Poty_coat.
                                                                                                                Pfam; PF00767; Poty_coat; 1.
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SEQUENCE 267 AA 2010 ...
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Best Local Similarity 66.7
Matches 4; Conservative
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SEQUENCE FROM N.A.
                              STRAIN-CHINESE;
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RA Amanatides P.G., Scherer S.E., Holf R. R., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P. W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P. W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RADIL J.F., Agbayari A., An H.-J., Androws-Ffannkoch C., Baldwin D.,
RADIL S.E., Bencos P.V., Berman B.P., Bhandari D., Blolahakov S.,
RADINGNO R., Doup L.E., Downes M., Dugard Rocha S., Dunkov B.C., Dunn P.,
RADINGNO R., Doup L.E., Downes M., Dugard Rocha S., Dunkov B.C., Dunn P.,
RADINGNO R., Doup L.E., Downes M., Dugard Rocha S., Dunkov B.C., Dunn P.,
RADINGNO R., Gabriellan A.E., Gatz N.S., Gelbart W.M., Glasser K.,
RADINGNO R., Gondriellan A.E., Gatz N.S., Gelbart W.M., Glasser R.,
RADINGNO R., Bouston R.A., Hovland T.J., Herrandez J.R., Houck J.,
RADILI M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Recthum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Recthum R.A.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RADINGLO R.M., Puttnan G.S., Pan S., Pollard J., Worsheri A.,
Radison D.R., Wallyn, Wunthy B., Murphy L., Murphy D.M., Walson D.R.,
Radison D.R., Pettman G.S., Pan S., Pollard J., Puri, V., Rese M.G.,
Rhenert K., Remington K.A., Nixon K., Nusskern D.,
Radisar R., Reinert K., Stanfards S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R. Yang Z.-Y., Wassarman D.A., Wolley K.C., Wu D., Yang S., Yao Q.A.,
R. Yang Z.-Y., Wassarman D.A., Wolley K.C., Wu D., Yang S., Zhu W., Saller P.,
R. Jang R., Zhong R., Rubin G.S., Zhu W., Salle R.,
R. Shirskas R., Wasser R., Rubin G.,
R. Shirskas R., Wasser R., Rubin G.,
R. Shirskas R., Wasser 
                                                                                                                                                Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Weoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                Last sequence update)
Last annotation update)
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InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
PRIMYS; PR001002; Y_phosphatase; 1.
PRNAT; SM00194; PTPC; 1.
PROSITE; PS00389; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
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HSSP; P28827; 1RPM.
01-MAY 2000 (TrEMBLrel. 13, 01-MAY 2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, CG14714 PROTEIN.
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Length 270;

DB 5;

Score 19;

90.58;

Query Match

71 EAGSAS 76

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Gaps

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Ma_L., Zhao Y., Wang J., Li J.;
"Sequence and function analysis of draTG genes downstream ORFs from Azospirillum brasilense Yu62.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF216815; AAF61911.1; --
InterPro; IPR003310; DNA_91ycosylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solc C.F., Derfler B.H., Duyk G.M., Corey D.P.;
"Molecular cloning of myosins from the bullfrog saccular macula: A candidate for the hair-cell adaptation motor.";
Aud. Neurosci. 163-75(1994).
ENBL: U14370; AAA55079.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
Azospirillum.
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 Length 287,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 2; Length 293; Pred. No. 1.6e+03; O; Mismatches 2; Indels
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                11 protein.
293 AA; 32063 MW; 37417EA008F6BD61 CRC64;
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                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 32.1 KDA PROTEIN.
AZOSPITILIUM brasilense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 Score 19; DB 13; L. Pred. No. 1.6e+03; 0; Mismatches 2;
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Pred. No. 1.7e+03;
                                                                                                                                                               293 AA
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Pfam; PF00063; myosin_head; 2.
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 90.58;
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66.78;
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                                4; Conservative
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297 AA;
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Best Local Similarity
Matches 4; Conserv
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                Best Local Similarity
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                                                                              110 EAGSTS 115
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|168 EAGAAS 173
                                                                                                                                                                                                                                                                                               NCBI_TaxID=192;
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SEQUENCE 29
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                  Gaps
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J. Biol. Cham. 272:29290-29300(1997).
EMBL; AF017299; AAC61897.1;
Interprop. IPR002101; MARCKS.
Pfam; PF02063; MARCKS.1.
PRINTS; PR00963; MARCKS.1.
PROSITE; PS00826; MARCKS.1;
PROSITE; PS00827; MARCKS.2; 1.
ROSITE; PS00827; MARCKS.2; 1.
SEQUENCE 287 AA; 29147 MW; 35CB7AE6090ED3C1 CRC64;
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MEDLINE-98030614; PubMed-9361009;
Shi Y., Sullivan S.K., Pitterle D.M., Kennington E.A., Graff J.M.,
                                                                                                                                                                                                                                  Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Pred. No. 1.6e+03;
); Mismatches 2; Indels
66.7%; Pred. No. 1.5e+03;
ive 0; Mismatches 2; Indels
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE.
MARCKS.
                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ICMF-LIKE PROTEIN (FRAGMENT).
                                                                                                                                               285 AA.
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 Best Local Similarity
Matches 4; Conserv
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210 EAGSAS 215
                                                             169 EAGSTS 174
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                                            1 eagxxs 6
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Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Borddin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camarco A.A., Camaroo D.M., Carraro D.M., Colution D.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
R. Fraqa J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
R. Fraqa J.S., Kuramae E.E., Langret F., Landbais M.R., Leite L.C.C.,
R. Hoper J.E., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
R. Krieger J.E., Kuramae E.E., Langret F., Landbais M.R., Leite L.C.C.,
R. Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marsuw G.L.,
R. Marques M.V., Martins E.A.L., Martins E.M.F., Marsuw G.L.,
R. Marques M.V., Martins E.A.L., Martins E.M.F., Marsuw A.Y.,
R. Marques M.V., Martins E.R.L., Martins C.L.,
R. Marques M.V., Nacilmento A.L.F.O., Netto L.E.S.,
R. Marques M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
R. Hanna A. Jr., Nobrega F.G., Pereira H.A. Jr., Pesquero J.B.,
R. Machado B.R., Pereira G.A., R.R., Oliveira M.A.,
R. A Silva A.M., de Sa R.G., Santelli R.V., Sawasaki H.E.,
R. A Silva A.C., A Sallva A.M., de Souza A.J.M.
A silva A.C.R., A Sallva A.M., de Souza A.D.,
R. A de Souza A.P., Terenzi M.F., Truffi D. Tsai S.M., Tsuhako M.H.,
R. Ago M.A., Zatz M., Meldanis J., Setubal J.C.;
R. The genome sequence of the plant pathogen Xylella fastidiosa.";
R. Parin, A. Perella C. Santelli R. P. M. Tsuhako M.H.,
R. The genome sequence of the plant pathogen Xylella fastidiosa.";
Gaps
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 Indels
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SEQUENCE 302 AA; 32047 MW; 758CC61DE4BE3590 CRC64;
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66.7%; Pred. No. 1.7e+03;
iive 0; Mismatches 2;
                                                                                                                           302 AA.
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MEDLINE=20365717; PubMed=10910347;
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(TrEMBLrel. 16, I
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 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Kataoka K., Fujiwara K.T., Noda M., Nishizawa M.;
"MafB,a new Maf family transcription activator that can associate with
GB|AAD26962.1.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryotá; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                           STRAIN-COLUMBIA;
MEDLINE-99087489; Pubmed-9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.";
DNA Res. 5.297-308199999999991.

EMBL: AB015473; BAB0839911; -.
SEQUENCE 307 AA; 35727 MW; 23CDB6C127CE90D1 CRC64;
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Mol. Cell. Biol. 14:7581-7591(1994).
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66.7%;
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Pfam; PF03131; bZIP_Maf; 1.
SMART; SMO0338; BRLZ; 1.
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Page 12

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SECUENCE FROM N.A.
TISSUE=BONE MARROW,
MEDLINE=99375320; PubMed=10444328;
Wang P.W., Eisenbart J.D., Cordes S.P., Barsh G.S., Stoffel M.,
Le Beau M.M.; Puman KRML (MAFB): cDNA cloning, genomic structure, and evaluation as a candidate tumor suppressor gene in myeloid leukemias.";
Genomics 59:275-281(1999).
EMBL; AF134157; AAD30106.1; -.
InterPro; IPR001871; bZIP.
Ffam; PF03131; bZIP.Maf; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HSP70 BINDING PROTEIN.
Brachydanio rerio (Zebrafish) (Zebra danio).
Brachydanio rerio (Zebrafish) (Zebra danio).
Actinopterygii; Nectezoa: Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human),
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ644L1.1 (KREISLER (MOUSE) MAR-RELATED LEUCINE ZIPPER HOMOLOG).
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EMBL; AL035665; CAB75863.1; -.
Interpro: IPR001871; bZIP.
SMART; SM0338; BRLZ: 1.
SEQUENCE 323 AA; 35792 MW; A0F3C09F8936CB16 CRC64;
                                                                                                                                                                                                                                                                                                323 AA; 35829 MW; AE4DC23408E36E55 CRC64;
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Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                NCBI_TaxID=9606;
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               Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                           SEQUENCE FROM N.A.
MEDLINE-96180718; Pubwed-8620536;
Sieweke M.H., Tekottte H., Frampton J., Graf T.;
"Maff is an interaction partner and repressor of Ets-1 that inhibits erythroid differentiation.";
                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21152895; PubMed=11231068; ISAIDSARIS. Y Sasuda K.; TSAIDSARI S., Yasuda K.; TSAIDSARI S., Yasuda K.; Tsaidsari S., Yasuda K.; Tasuda K.; Toles of maf genes during Xenopus lens development."; Mech. Dev. 101:155-166(2001). EMBL: AF202058; AAF08316.1; -. InterPro: IPROUB71; bZIP. Pfam: PF03131; bZIP. Maf; 1. SMART; SM00338; BRLZ; 1.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MAFB/KREISLER BASIC REGION/LEUGINE ZIPPER TRANSCRIPTION FACTOR.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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EMBL: X95511; CAA65360.1; -
InterPro: IPR001871; bZIP.
Pfam: PF01131; bZIP_Maf; 1.
SMART; SM00338; BRLZ; 1.
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Best Local Similarity
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Matches 4; Conserv
                                                                            NCBI_TaxID=93934;
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298 EAGSTS 303
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09Y5Q3;
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2; Indels

Length 350;

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SEQUENCE FROM N.A.
STRAIN=MAFF303099;
MEDLINE=21082930;
PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishikawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.,
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Puehler A.,
The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL, ALG03642; CAC4647.1;
Plasmid, Hypothetical protein; Complete proteome.
SEQUENCE 352 AA; 37018 MW; F4AEG710196E06EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pSymB (megaplasmid 2).

Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae: Sinorhizobium.
NCBL_TaxID-3182;
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DNA Res. 7:331-338(2000).

EMBL: APPO3016: BABS4976.1; -.

Plasmid; Complete proteome.

SEQUENCE 350 AA; 39172 MW; BB075F9345BB9362 CRC64;
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Pred. No. 2e+03;
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
PUTATIVE ADENYLATE CYCLASE PROFEIN.
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Conservative
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Best Local Similarity
Matches 4; Conserv
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Arundinelleae; Arundinella.
                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium loti (Mesorhizobium loti).
Plasmid pMLa.
Bacteria: Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
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Pred. No. 1.9e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                       90.5%; Score 19; DB 13; Length 333;
66.7%; Pred. No. 1.9e+03;
Live 0; Mismatches 2; Indels
                                                        Guerriero V., Raynes D.A.;
Hap70 binding protein from zebra fish (HspBPF).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY024356; AAG61257.1, ...
InterPro: IPR000225; Armadillo.
Ffam: PF00514; Armadillo.seg; 2.
SWART; SMO0185; ARM; 2.
SEQUENCE 333 AA; 37269 WW; E7C5ABD12F41D23E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 AA; 36902 MW; BFB5F29CD7449C89 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TEOSINTE BRANCHEDI PROTEIN (FRAGMENT).
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EMBL; AF322131; AAK37493.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=21165336; PubMed=11264415;
Cypriniformes; Cyprinidae; Danio.
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Similarity 66.7%;
4; Conservative
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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"Direct Submission.";
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Best Local Similarity
Matches 4; Conserv
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MEDLINE-98165393; PubMed-9425134;
Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;
"Equivalence in the genetic control of hindbrain segmentation in fish
                                                                                                                                                                                                                                   Gaps
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                                                                                                    "Isolation, Characterization, and Expression Analysis of Zebrafish Large Mafs.";
Jusque Mafs.";
Jusque Mafs.";
EMBL, 38006322; BAB21102.1;
EMBL, AB006322; BRB21102.1;
Pfant. PF03131; bZIP.
Pfan: PF03131; bZIP.Maf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
Brachydanio rerio (Zebrafish) (Zebra danio).
Wataryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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                                                                       MEDLINE-21064923; PubMed-11134968;
Kajihara M., Kawauchi S., Kobayashi M., Ogino H., Takahashi
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Pred. No. 2e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                              40233 MW; DE4C96B62C058865 CRC64;
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Pfam; PF03131; DZIP.Maf; 1.
SMART; SM00338; BRLZ; 1.
SEQUENCE 356 AA; 40243 MW; 07420DB0F6CD08F1 CRC64;
                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-BC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSCRIPTION FACTOR VAL.
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Last sequence update)
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EMBL; AF006641; AAC18821.1; -.
ZFIN; ZDB-GENE-980526-515; val.
                                                                                                                                                                                                           90.5%;
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                                                                                                                                                                             356 AA;
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Best Local Similarity
Matches 4; Conserv
                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                       Best Local Similarity
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                                         NCBI_TaxID=7955;
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01-JAN-1998
                                                                                           Yasuda K.;
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Arabidopsis thallana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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STRAIN-BRISTOL N2;
Bemis G., Lamar B., Courtney L., Wohldmann P., Harrison M.;
"The sequence of C. elegans cosmid Y18H1A.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 357;
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STRAIN-CV. COLUMBIA;
Dempsey S., Harper M.,
The sequence of A. thaliana TM018A10.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERAIM-CV. COLUMBIA;
Waterston R.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF013294; AAB62869.1; -.
InterPro; IPR001810; F-box.
Pfam; PF00046; Fbox; 1.
SMART; SM00256; FBOX; 1.
SEQUENCE 357 AA; 40078 MW; B1683A07BF630633 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The A. thaliana Genome Sequencing Project.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) A_TM018A10.10 PROTEIN. A_TM018A10.10.
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TISSUE-SKELETAL MUSCLE;

TISSUE-SKELETAL MUSCLE;

MEDLINE-20409785; PubMed=11034912;

MEDLINE-20409785; PubMed=11034912;

Antisense oligonucleotide experiments elucidate the essential role of titin in sarcomerogenesis in adult rat cardiomyocytes in long-term titin in sarcomerogenesis in adult rat cardiomyocytes in long-term culture.;

T. Cell Sci. 113:3851-3859(2000).

EMBL; AJ401157; CAB95001.1; -...

BEL; AJ401157; CAB95001.1; -...

RINEPPRO; IPR003600; Ig_like.

InterPro; IPR003600; Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
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90.5%; Score 19; DB 11; Length 362;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                         90.5%; Score 19; DB 5; Length 361;
66.7%; Pred. No. 2e+03;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AC024751; AAK21510.1; -. Hypothetical protein. SEQUENCE 361 AA; 40201 MW; 98F44C3F87D59625 CRC64;
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39601 MW; E8E6CE65BB7F4ED8 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                               362 AA.
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01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
TITIN (FRAGMENT).
                                                                                            Query Match
Best Local Similarity 66.73
Matches 4; Conservative
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NON_TER 362 362
SEQUENCE 362 AA; 39
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Search completed: August 30, 2002, 15:11:35 Job time: 346 sec

